

**RNA INTERFERENCE MEDIATED INHIBITION OF HEPATITIS C VIRUS  
(HCV) GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID  
(siNA)**

This invention is a continuation-in-part of McSwiggen 10/444,853 filed May 23,  
5 2003 and a continuation-in-part of McSwiggen PCT/US03/05043 filed February 20,  
2003, which is a continuation-in-part of McSwiggen PCT/US02/09187 filed March 26,  
2002, and claims the benefit of McSwiggen USSN 60/401,104 filed August 5, 2002, of  
Beigelman USSN 60/358,580 filed February 20, 2002, of Beigelman USSN 60/363,124  
filed March 11, 2002, of Beigelman USSN 60/386,782 filed June 6, 2002, of Beigelman  
10 USSN 60/406,784 filed August 29, 2002, of Beigelman USSN 60/408,378 filed  
September 5, 2002, of Beigelman USSN 60/409,293 filed September 9, 2002, and of  
Beigelman USSN 60/440,129 filed January 15, 2003. The instant application claims  
priority to all of the listed applications, which are hereby incorporated by reference  
herein in their entireties, including the drawings.

15 Field Of The Invention

The present invention concerns compounds, compositions, and methods for the  
study, diagnosis, and treatment of conditions and diseases that respond to the modulation  
of hepatitis C virus (HCV) gene expression and/or activity. The present invention also  
concerns compounds, compositions, and methods relating to conditions and diseases that  
20 respond to the modulation of expression and/or activity of genes involved in HCV  
pathways. Specifically, the invention relates to small nucleic acid molecules, such as  
short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded  
RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules  
capable of mediating RNA interference (RNAi) against hepatitis C virus (HCV) gene  
25 expression.

Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is  
provided only for understanding of the invention that follows. The summary is not an  
admission that any of the work described below is prior art to the claimed invention.

RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806, Hamilton *et al.*, 1999, *Science*, 286, 950-951). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Hamilton *et al.*, *supra*; Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Hamilton *et al.*, *supra*; Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Bahramian and Zarbl, 1999, *Molecular and Cellular Biology*, 19, 274-283 and Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mammalian systems. Hammond *et al.*, 2000, 5 *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877) has revealed certain requirements for siRNA length, structure, 10 chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 15 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'- 20 phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two nucleotide 3'-overhangs with 25 deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). In addition, Elbashir *et al.*, *supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely 30 abolishes RNAi activity. Li *et al.*, International PCT Publication No. WO 00/44914, and Beach *et al.*, International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither

application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in siRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, tested certain chemical modifications targeting the unc-22 gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified bases also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi system and the use of specific siRNA molecules for certain functional genomic and



certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO 00/44914, describe the use of specific dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian cells using certain dsRNA molecules. Fire *et al.*, International PCT Publication No. WO 99/32619, describe particular methods for introducing certain dsRNA molecules into cells for use in inhibiting gene expression. Plaetinck *et al.*, International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific dsRNA molecules. Mello *et al.*, International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.*, International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse *et al.*, International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll *et al.*, International PCT Publication No. WO 01/49844, describe specific DNA constructs for use in facilitating gene silencing in targeted organisms.

Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, describe specific chemically-modified siRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov *et al.*, International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.*, International PCT Publication No. WO 01/53475, describe certain methods for isolating a *Neurospora* silencing gene and uses thereof. Reed *et al.*, International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.*, International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak *et al.*, International PCT Publication No. WO 01/72774, describe certain

*Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.*, International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.*, International PCT Publication No. WO 02/44321, describe certain synthetic siRNA  
5 constructs. Pachuk *et al.*, International PCT Publication No. WO 00/63364, and Satishchandran *et al.*, International PCT Publication No. WO 01/04313, describe certain methods and compositions for inhibiting the function of certain polynucleotide sequences using certain dsRNAs. Echeverri *et al.*, International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.*,  
10 International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using RNAi. Graham *et al.*, International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.*, US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain certain long dsRNA  
15 (greater than 25 nucleotide) constructs that mediate RNAi. Harborth *et al.*, 2003, Antisense & Nucleic Acid Drug Development, 13, 83-105, describe certain chemically and structurally modified siRNA molecules. Chiu and Rana, 2003, RNA, 9, 1034-1048, describe certain chemically and structurally modified siRNA molecules.

McCaffrey *et al.*, 2002, *Nature*, 418, 38-39, describes the use of certain siRNA  
20 constructs targeting a chimeric HCV NS5B protein/luciferase transcript in mice.

Randall *et al.*, 2003, *PNAS USA*, 100, 235-240, describe certain siRNA constructs targeting HCV RNA in Huh7 hepatoma cell lines.

## SUMMARY OF THE INVENTION

This invention relates to compounds, compositions, and methods useful for  
25 modulating the expression of genes, such as those genes associated with the development or maintenance of HCV infection, liver failure, hepatocellular carcinoma, cirrhosis, and/or other disease states associated with HCV infection, by RNA interference (RNAi) using short interfering nucleic acid (siNA) molecules. This invention also relates to compounds, compositions, and methods useful for modulating the expression and  
30 activity of hepatitis C virus (HCV), or genes involved in hepatitis C virus (HCV) gene expression and/or activity by RNA interference (RNAi) using small nucleic acid

molecules. In particular, the instant invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of hepatitis C virus (HCV). A  
5 siNA of the invention can be unmodified or chemically-modified. A siNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-modified synthetic short interfering nucleic acid (siNA) molecules capable of modulating hepatitis C virus gene expression or activity in cells by RNA interference (RNAi). The use of chemically-  
10 modified siNA improves various properties of native siNA molecules through increased resistance to nuclease degradation *in vivo* and/or through improved cellular uptake. Further, contrary to earlier published studies, siNA having multiple chemical modifications retains its RNAi activity. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, target  
15 validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of gene(s) encoding the hepatitis C virus. Specifically, the present invention features siNA molecules that modulate the expression of HCV proteins, for example, proteins encoded  
20 by sequences shown as Genbank Accession Nos. in Table I.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a HCV RNA, wherein said siNA molecule comprises about 19 to about 21 base pairs.

In one embodiment, the invention features siNA molecules having RNAi  
25 specificity for the HCV minus strand, for example, Genbank Accession No. HPCCK1S1, Hepatitis C virus (strain HCV-1b, clone HCV-K1-S1), complete genome; Genbank Accession No. D50483, 9410 nt.

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of genes  
30 representing cellular targets for HCV infection, such as cellular receptors, cell surface molecules, cellular enzymes, cellular transcription factors, and/or cytokines, second

messengers, and cellular accessory molecules including, but not limited to, interferon regulatory factors (IRFs; e.g., Genbank Accession No. AF082503.1); cellular PKR protein kinase (e.g., Genbank Accession No. XM\_002661.7); human eukaryotic initiation factors 2B (eIF2Bgamma; e.g., Genbank Accession No. AF256223, and/or  
 5 eIF2gamma; e.g., Genbank Accession No. NM\_006874.1); human DEAD Box protein (DDX3; e.g., Genbank Accession No. XM\_018021.2); and cellular proteins that bind to the poly(U) tract of the HCV 3'-UTR, such as polypyrimidine tract-binding protein (e.g., Genbank Accession Nos. NM\_031991.1 and XM\_042972.3).

Due to the high sequence variability of the HCV genome, selection of siNA  
 10 molecules for broad therapeutic applications would likely involve the conserved regions of the HCV genome. In one embodiment, the present invention relates to siNA molecules that target the conserved regions of the HCV genome. Examples of conserved regions of the HCV genome include, but are not limited to, the 5'-Non Coding Region (NCR, also referred to as 5'-untranscribed region, UTR), the 5'-end of the core protein  
 15 coding region, and the 3'- NCR. HCV genomic RNA contains an internal ribosome entry site (IRES) in the 5'-NCR which mediates translation independently of a 5'-cap structure (Wang *et al.*, 1993, *J. Virol.*, 67, 3338-44). The full-length sequence of the HCV RNA genome is heterologous among clinically isolated subtypes, of which there are at least fifteen (Simmonds, 1995, *Hepatology*, 21, 570-583), however, the 5'-NCR  
 20 sequence of HCV is highly conserved across all known subtypes, most likely to preserve the shared IRES mechanism (Okamoto *et al.*, 1991, *J. General Virol.*, 72, 2697-2704). Therefore, a siNA molecule can be designed to target the different isolates of HCV by targeting a conserved region, such as the 5' NCR sequence. siNA molecules designed to target conserved regions of various HCV isolates enable efficient inhibition of HCV  
 25 replication in diverse patient populations and ensure the effectiveness of the siNA molecules against HCV quasi species which evolve due to mutations in the non-conserved regions of the HCV genome. As described, a single siNA molecule can be targeted against all isolates of HCV by designing the siNA molecule to interact with conserved nucleotide sequences of HCV (e.g., sequences that are expected to be present  
 30 in the RNA of various HCV isolates).

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of gene(s)

encoding HCV and/or cellular proteins associated with the maintenance or development of HCV infection, liver failure, hepatocellular carcinoma, and cirrhosis, such as genes encoding sequences comprising those sequences referred to by GenBank Accession Nos. shown in **Table I**, referred to herein generally as HCV. The description below of the various aspects and embodiments of the invention is provided with reference to exemplary hepatitis C virus (HCV) genes, generally referred to herein as HCV. However, such reference is meant to be exemplary only and the various aspects and embodiments of the invention are also directed to other genes that express alternate HCV genes, such as mutant HCV genes, splice variants of HCV genes, and genes encoding different strains of HCV, as well as as cellular targets for HCV, such as those described herein. The various aspects and embodiments are also directed to other genes involved in HCV pathways, including genes that encode cellular proteins involved in the maintenance and/or development of HCV infection, liver failure, hepatocellular carcinoma, and cirrhosis or other genes that express other proteins associated with HCV infection, such as cellular proteins that are utilized in the HCV life-cycle. Such additional genes can be analyzed for target sites using the methods described herein for HCV. Thus, the inhibition and the effects of such inhibition of the other genes can be performed as described herein. In other words, the term “HCV” as it is defined herein below and recited in the described embodiments, is meant to encompass genes associated with the development and/or maintenance of HCV infection, such as genes which encode HCV polypeptides, including polypeptides of different strains of HCV, mutant HCV genes, and splice variants of HCV genes, as well as cellular genes involved in HCV pathways of gene expression, replication, and/or HCV activity. Also, the term “HCV” as it is defined herein below and recited in the described embodiments, is meant to encompass HCV viral gene products and cellular gene products involved in HCV infection, such as those described herein. Thus, each of the embodiments described herein with reference to the term “HCV” are applicable to all of the virus, cellular and viral protein, peptide, polypeptide, and/or polynucleotide molecules covered by the term “HCV”, as that term is defined herein.

30 In one embodiment, the invention features a siNA molecule that down-regulates expression of a HCV gene, for example, wherein the HCV gene comprises HCV encoding sequence or a portion thereof.



In one embodiment, the invention features a siNA molecule having RNAi activity against HCV RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having HCV or other HCV encoding sequence, such as those sequences having GenBank Accession Nos. shown in **Table I**. Chemical modifications as shown in  
 5 **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the invention.

In one embodiment, the invention features a siNA molecule having RNAi activity against HCV RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having HCV encoding sequence, such as those sequences having HCV  
 10 GenBank Accession Nos. shown in **Table I**. Chemical modifications as shown in **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the invention.

In another embodiment, the invention features a siNA molecule having RNAi activity against a HCV gene, wherein the siNA molecule comprises nucleotide sequence  
 15 complementary to nucleotide sequence of a HCV gene, such as those HCV sequences having GenBank Accession Nos. shown in **Table I**. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a HCV gene and thereby mediate silencing of HCV gene expression, for example, wherein the siNA mediates regulation of HCV gene expression by cellular  
 20 processes that modulate the chromatin structure of the HCV gene and prevent transcription of the HCV gene.

In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the siNA molecule that is complementary to a nucleotide sequence of a HCV gene or portion  
 25 thereof. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence comprising a HCV gene sequence or portion thereof.

In one embodiment, the antisense region of HCV siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1-696, 1393-1413, or  
 30 1606-1612. In one embodiment, the antisense region can also comprise sequence having any of SEQ ID NOs. 697-1392, 1414, 1418, 1420, 1428-1434, 1456-1462, 1479, 1483,

1489-1491, 1493, 1497-1498, 1633-1636, 1658-1681, 1698, 1700, 1702, or 1705. In another embodiment, the sense region of HCV constructs can comprise sequence having any of SEQ ID NOs. 1-696, 1393-1411, 1606-1612, 1413, 1417, 1419, 1421-1427, 1449-1455, 1477-1478, 1481-1482, 1485-1488, 1494-1496, 1499, 1501-1512, 1549, 1553, 5 1558-1569, 1613-1616, 1629-1632, 1645-1647, 1651, 1653, 1655-1657, 1658-1681, 1697, 1699, 1701, 1703, or 1704. The sense region can comprise a sequence of SEQ ID NO. 1688 and the antisense region can comprise a sequence of SEQ ID NO. 1689. The sense region can comprise a sequence of SEQ ID NO. 1690 and the antisense region can comprise a sequence of SEQ ID NO. 1691. The sense region can comprise a sequence of 10 SEQ ID NO. 1692 and the antisense region can comprise a sequence of SEQ ID NO. 1693. The sense region can comprise a sequence of SEQ ID NO. 1694 and the antisense region can comprise a sequence of SEQ ID NO. 1691. The sense region can comprise a sequence of SEQ ID NO. 1695 and the antisense region can comprise a sequence of SEQ ID NO. 1691. The sense region can comprise a sequence of SEQ ID NO. 1694 and the 15 antisense region can comprise a sequence of SEQ ID NO. 1696.

In one embodiment, a siNA molecule of the invention comprises any of SEQ ID NOs. 1-1681 or 1688-1705. The sequences shown in SEQ ID NOs: 1-1681 and 1688-1705 are not limiting. A siNA molecule of the invention can comprise any contiguous HCV sequence (e.g., about 19 to about 25, or about 19, 20, 21, 22, 23, 24 or 25 20 contiguous HCV nucleotides).

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank Accession Nos. shown in **Table I**. Chemical modifications in **Tables III and IV** and 25 described herein can be applied to any siRNA construct of the invention.

In one embodiment of the invention a siNA molecule comprises an antisense strand having about 19 to about 29 nucleotides (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29), wherein the antisense strand is complementary to a RNA sequence encoding a HCV protein, and further comprises a sense strand having about 19 to about 30 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the sense strand and the antisense strand are distinct nucleotide sequences with at least about 19 complementary nucleotides.

In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the antisense region is complementary to a RNA sequence encoding a HCV protein, and further comprises a sense region having  
5 about 19 to about 29 nucleotides (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29), wherein the sense region and the antisense region comprise a linear molecule with at least about 19 complementary nucleotides.

In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence  
10 encoding a HCV protein or a portion thereof. The siNA further comprises a sense strand, wherein the sense strand comprises a nucleotide sequence of a HCV gene or a portion thereof.

In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence  
15 encoding a HCV protein or a portion thereof. The siNA molecule further comprises a sense region, wherein the sense region comprises a nucleotide sequence of a HCV gene or a portion thereof.

In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a HCV gene. Because HCV genes can share  
20 some degree of sequence homology with each other, siNA molecules can be designed to target a class of HCV genes or alternately specific HCV genes by selecting sequences that are either shared amongst different HCV targets or alternatively that are unique for a specific HCV target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of HCV RNA sequence having homology between several  
25 HCV genes so as to target several HCV genes (e.g., different HCV isoforms, splice variants, mutant genes etc.) with one siNA molecule. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific HCV RNA sequence due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

30 In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid

molecules. In another embodiment, the siNA molecules of the invention consist of duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24 or 25) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplexes with overhanging ends of about about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotides, for example about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs.

In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for HCV expressing nucleic acid molecules, such as RNA encoding a HCV protein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical modifications, when used in various siNA constructs, are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al.*, *supra*, applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA constructs.

In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (*e.g.*, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA

molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand. In one embodiment, the HCV RNA comprises HCV minus strand RNA. In another embodiment, the HCV RNA comprises HCV plus strand RNA.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof, and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, all of the pyrimidine nucleotides present in the double-stranded siNA molecule comprise a sugar modification. In one embodiment, each strand of the double-stranded siNA molecule comprises about 19 to about 29 nucleotides and each strand comprises at least about 19 nucleotides that are complementary to the nucleotides of the other strand. In another embodiment, the double-stranded siNA molecule is assembled from two oligonucleotide fragments, wherein one fragment comprises nucleotide sequence of the antisense strand of the siNA molecule and the second fragment comprises nucleotide sequence of the sense strand of the siNA molecule. In yet another embodiment, the sense strand of the double-stranded siNA molecule is connected to the antisense strand via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker. In another embodiment, any pyrimidine nucleotides (i.e., one or more or all) present in the sense strand of the double-stranded siNA molecule are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides (i.e., one or more or all) present in the sense



region are 2'-deoxy purine nucleotides. In yet another embodiment, the sense strand of the double-stranded siNA molecule comprises a 3'-end and a 5'-end, wherein a terminal cap moiety (e.g., an inverted deoxy abasic moiety or inverted deoxy nucleotide moiety such as inverted thymidine) is present at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the sense strand. In another embodiment, the antisense strand of the double-stranded siNA molecule comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides and one or more 2'-O-methyl purine nucleotides. In yet another embodiment, any pyrimidine nucleotides present in the antisense strand of the double-stranded siNA molecule are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-O-methyl purine nucleotides. In another embodiment, the antisense strand of the double-stranded siNA molecule comprises a phosphorothioate internucleotide linkage at the 3' end of the antisense strand. In yet another embodiment, the antisense strand comprises a glyceryl modification at the 3' end of the antisense strand. In still another embodiment, the 5'-end of the antisense strand optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein each of the two strands of said siNA molecule comprises 21 nucleotides. In one embodiment, 21 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the HCV RNA or a portion thereof. In another embodiment, about 19 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the HCV RNA or a portion thereof. In one embodiment, each strand of the siNA molecule is base-paired to the complementary nucleotides of the other strand of the siNA molecule. In another embodiment, about 19 nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule and at least two 3' terminal nucleotides of each strand of the siNA molecule are not base-paired to the nucleotides of the other strand of the siNA molecule. In one embodiment, each of

the two 3' terminal nucleotides of each strand of the siNA molecule that are not base-paired are 2'-deoxy-pyrimidines, such as 2'-deoxy-thymidine.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV),  
5 wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-  
10 stranded siNA molecule comprises a sugar modification and wherein the nucleotide sequence of the antisense strand or a portion thereof is complementary to a nucleotide sequence of the 5'-untranslated region of an HCV RNA or a portion thereof.

In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV),  
15 wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof, and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-  
20 stranded siNA molecule comprises a sugar modification and wherein the nucleotide sequence of the antisense strand or a portion thereof is complementary to a nucleotide sequence of an HCV RNA that is present in the RNA of all HCV.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a HCV RNA comprising  
25 a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of HCV RNA or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the siNA molecule has one or more modified pyrimidine and/or purine nucleotides. In one embodiment, the pyrimidine  
30 nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides or 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides in the

sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In one embodiment, the pyrimidine nucleotides in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the antisense region are 2'-O-methyl or 2'-deoxy purine nucleotides. In another embodiment of any of the above described siNA molecules, any nucleotides present in a non-complementary region of the sense strand (e.g. overhang region) are 2'-deoxy nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to the nucleotide sequence of an RNA encoding a HCV protein or a fragment thereof and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand. In one embodiment, a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein the fragment comprising the sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the fragment comprising the sense region. In another embodiment, the terminal cap moiety is an inverted deoxy abasic moiety or glyceryl moiety. In another embodiment, each of the two fragments of the siNA molecule comprise about 21 nucleotides.

In one embodiment, the invention features a siNA molecule comprising at least one modified nucleotide, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. The siNA can be, for example, of length between about 12 and about 36 nucleotides. In

another embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least  
5 one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In another embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In another  
10 embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as phosphorothioate linkage. In another embodiment, the 2'-deoxy-2'-fluoronucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine  
15 nucleotides. In another embodiment, the siNA comprises a sequence that is complementary to a nucleotide sequence in a separate RNA, such as a viral RNA (e.g., HCV RNA).

In one embodiment, the invention features a method of increasing the stability of a siNA molecule against cleavage by ribonucleases comprising introducing at least one  
20 modified nucleotide into the siNA molecule, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. In another embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in  
25 the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In another embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro  
30 adenosine nucleotides. In another embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as phosphorothioate linkage. In another embodiment, the 2'-deoxy-2'-fluoronucleotides are present at specifically selected

locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV) comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof of HCV and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the purine nucleotides present in the antisense region comprise 2'-deoxy- purine nucleotides. In an alternative embodiment, the purine nucleotides present in the antisense region comprise 2'-O-methyl purine nucleotides. In either of the above embodiments, the antisense region can comprise a phosphorothioate internucleotide linkage at the 3' end of the antisense region. Alternatively, in either of the above embodiments, the antisense region can comprise a glyceryl modification at the 3' end of the antisense region. In another embodiment of any of the above described siNA molecules, any nucleotides present in a non-complementary region of the antisense strand (e.g. overhang region) are 2'-deoxy nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In one embodiment about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule, wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine nucleotide, such as a 2'-deoxy-thymidine. In another embodiment, all 21 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence of the HCV RNA or a portion thereof. In another embodiment, about 21 nucleotides of the antisense region are



base-paired to the nucleotide sequence of the HCV RNA or a portion thereof. In any of the above embodiments, the 5'-end of the fragment comprising said antisense region can optionally include a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of a hepatitis C virus (HCV), wherein the siNA molecule does not contain any ribonucleotides and wherein each strand of the double-stranded siNA molecule is about 21 nucleotides long. Examples of non-ribonucleotide containing siNA constructs are combinations of stabilization chemistries shown in Table IV in any combination of Sense/Antisense chemistries, such as Stab 7/8, Stab 7/11, Stab 8/8, Stab 18/8, Stab 18/11, Stab 12/13, Stab 7/13, or Stab 18/13.

In one embodiment, the invention features a pharmaceutical composition comprising a siNA molecule of the invention in an acceptable carrier or diluent.

In one embodiment, the invention features a medicament comprising an siNA molecule of the invention.

In one embodiment, the invention features an active ingredient comprising an siNA molecule of the invention.

In one embodiment, the nucleotide sequence of the antisense strand or a portion thereof of a siNA molecule of the invention is complementary to the nucleotide sequence of an HCV RNA or a portion thereof that is present in the RNA of all HCV isolates.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule that inhibits replication of a hepatitis C virus (HCV), wherein one of the strands of said double-stranded siNA molecule is an antisense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of an HCV RNA or a portion thereof and the other strand is a sense strand which comprises a nucleotide sequence that is complementary to the nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in said double-stranded siNA molecule comprises a sugar modification.

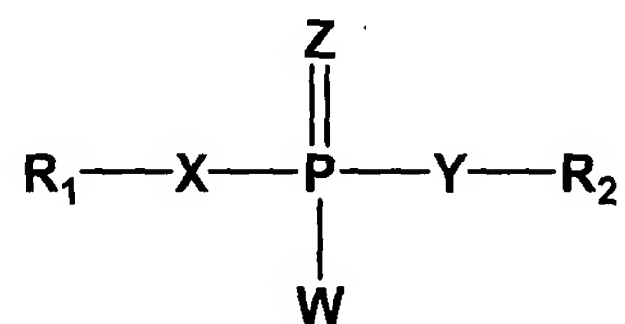
In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity in humans.

In any of the embodiments of siNA molecules described herein, the antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can

comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding HCV and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:

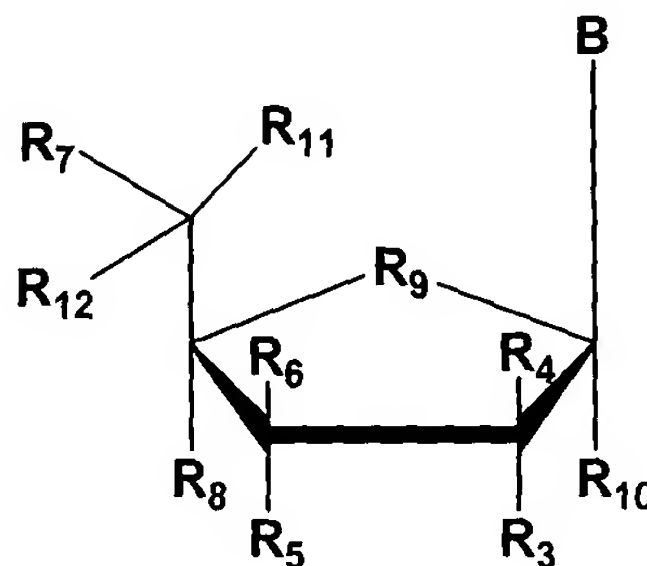


wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or acetyl and wherein W, X, Y, and Z are optionally not all O. In another embodiment, a backbone modification of the invention comprises a phosphonoacetate and/or thiophosphonoacetate internucleotide linkage (see for example Sheehan et al., 2003, Nucleic Acids Research, 31, 4109-4118).

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In

another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example,  
 5 an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide  
 10 or non-nucleotide having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or  
 15 non-nucleotides having Formula II:

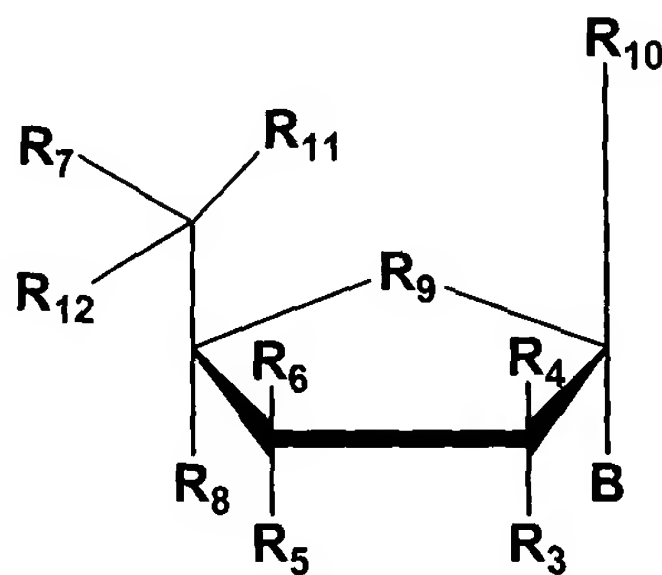


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH,  
 20 O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-  
 25 aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine,

pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:



20

wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF<sub>3</sub>, OCF<sub>3</sub>, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO<sub>2</sub>, NO<sub>2</sub>, N<sub>3</sub>, NH<sub>2</sub>, aminoalkyl, aminoacid, aminoacyl, ONH<sub>2</sub>, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino,

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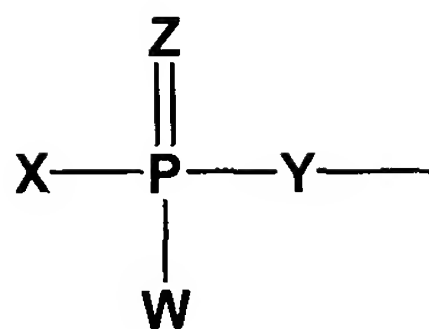


substituted silyl, or group having Formula I or II; R<sub>9</sub> is O, S, CH<sub>2</sub>, S=O, CHF, or CF<sub>2</sub>, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to  
 5 target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the  
 10 sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-  
 15 modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

20 In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

25 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, alkylhalo, or acetyl; and wherein W, X, Y and Z are not all O.

5           In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand, for example, a strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary  
10 strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-complementary strand of a siNA molecule of the invention, for example a siNA  
15 molecule having chemical modifications having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a  
20 non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA  
25 strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an

exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*,  
 5 about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

10 In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and  
 15 optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3,  
 20 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides,  
 25 with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate  
 30 internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end,

the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*,  
5 about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro  
10 nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a siNA molecule, wherein the antisense  
15 strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends  
20 of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a  
25 terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more  
30 phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more  
 5 (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl,  
 10 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-  
 15 modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a chemically-modified short interfering  
 20 nucleic acid (siNA) molecule having about 1 to about 5, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the  
 25 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in  
 30 one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-



modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification comprises a structure having any of Formulae I-VII. For example, an exemplary

5 chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of

10 the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-

15 modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another

20 embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2

25 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 25 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,

30 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (*e.g.*, about

25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 3 to about 23 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, a linear hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

In another embodiment, a siNA molecule of the invention comprises an asymmetric hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 20 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms an asymmetric hairpin structure having about 3 to about 18 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, an asymmetric hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, an asymmetric hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

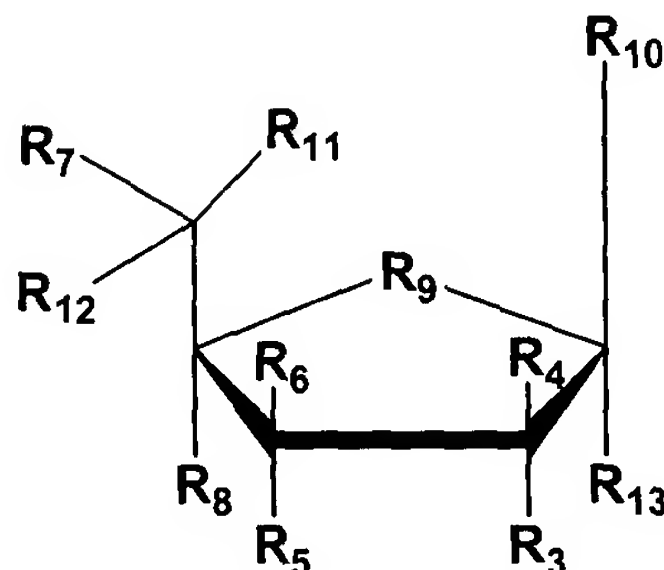
In another embodiment, a siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 16 to about 25 (*e.g.*, about 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides in length, wherein the sense

region is about 3 to about 18 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides in length, wherein the sense region the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 18 to about 22 (*e.g.*, about 18, 19, 20, 21, or 22) nucleotides in length and wherein the sense region is about 3 to about 15 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15) nucleotides in length, wherein the sense region the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. In another embodiment, the asymmetric double stranded siNA molecule can also have a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV).

In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

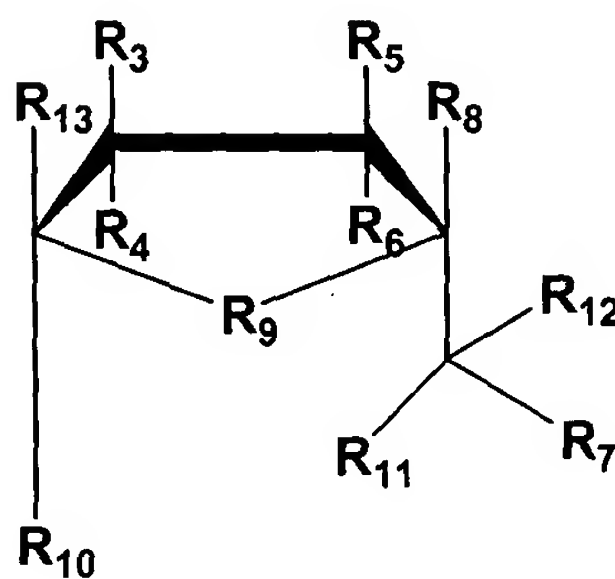
In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



- 5 wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid,  
 10 O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:

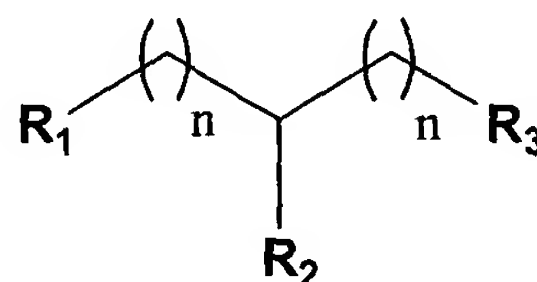


15

- wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2,  
 20 NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid,

O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R<sub>9</sub> is O, S, CH<sub>2</sub>, S=O, CHF, or CF<sub>2</sub>, and either R<sub>2</sub>, R<sub>3</sub>, R<sub>8</sub> or R<sub>13</sub> serve as points of attachment to the siNA molecule of the invention.

- 5 In another embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



- wherein each *n* is independently an integer from 1 to 12, each R<sub>1</sub>, R<sub>2</sub> and R<sub>3</sub> is  
 10 independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF<sub>3</sub>, OCF<sub>3</sub>, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO<sub>2</sub>, NO<sub>2</sub>, N<sub>3</sub>, NH<sub>2</sub>, aminoalkyl, aminoacid, aminoacyl, ONH<sub>2</sub>, O-  
 aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl,  
 15 aminoalkylamino, polyalkylamino, substituted silyl, or a group having Formula I, and R<sub>1</sub>, R<sub>2</sub> or R<sub>3</sub> serves as points of attachment to the siNA molecule of the invention.

- In another embodiment, the invention features a compound having Formula VII, wherein R<sub>1</sub> and R<sub>2</sub> are hydroxyl (OH) groups, *n* = 1, and R<sub>3</sub> comprises O and is the  
 20 point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in **Figure 10**).

- In another embodiment, a moiety having any of Formula V, VI or VII of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of  
 25 the invention. For example, a moiety having Formula V, VI or VII can be present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.



In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

5 In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

10 In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA  
15 comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-  
20 deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA  
25 comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-  
30 deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine

nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any  
 5 (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or more or all)  
 10 purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any  
 (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-  
 15 2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or more or all)  
 purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a  
 20 plurality of purine nucleotides are 2'-O-methyl purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein  
 25 any (e.g., one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine  
 30 nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are  
 5 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), wherein  
 10 any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are  
 15 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or  
 20 alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are  
 25 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

30 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against HCV inside a cell or reconstituted *in vitro* system comprising a sense

region, wherein one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more

5 purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and an antisense region, wherein one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro

10 pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). The sense region and/or the antisense

15 region can have a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense and/or antisense sequence. The sense and/or antisense region can optionally further comprise a 3'-terminal nucleotide overhang having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) 2'-deoxynucleotides. The overhang nucleotides can

20 further comprise one or more (*e.g.*, about 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Tables III and IV** herein. In any of these described embodiments, one or more of the purine nucleotides present in the sense region are alternatively 2'-O-methyl purine nucleotides

25 (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides) and one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Also, in any of these

30 embodiments, one or more purine nucleotides present in the sense region are alternatively purine ribonucleotides (*e.g.*, wherein all purine nucleotides are purine ribonucleotides or alternately a plurality of purine nucleotides are purine ribonucleotides) and any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or

alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Additionally, in any of these embodiments, one or more purine nucleotides present in the sense region and/or present in the antisense region are alternatively selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides). In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides. In any of the embodiments, the sense strand of a double stranded siNA molecule of the invention comprises a terminal cap moiety, (see for example **Figure 10**) such as an inverted deoxyabaisc moiety, at the 3'-end, 5'-end, or both 3' and 5'-ends of the sense strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) against HCV inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule.



Non-limiting examples of conjugates contemplated by the invention include conjugates and ligands described in Vargeese *et al.*, USSN 10/427,160, filed April 30, 2003, incorporated by reference herein in its entirety, including the drawings. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate molecule attached to the chemically-modified siNA molecule is a poly ethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.*, U.S. Serial No. 10/201,394, incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of  $\geq 2$  nucleotides in length, for example about 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a

nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid.

5 The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.*, 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those  
15 having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma *et al.*, *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand *et al.*, *Nucleic Acids Res.* 1990, 18:6353; McCurdy *et al.*, *Nucleosides & Nucleotides* 1991, 10:287; Ischke *et al.*, *Tetrahedron Lett.* 1993, 34:301; Ono *et al.*, *Biochemistry* 1991, 30:9914; Arnold *et al.*, International Publication No. WO 89/02439; Usman *et al.*, International Publication No. WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz  
25 and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not  
30 contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. For example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA comprise separate oligonucleotides not having any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotides. In another example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA are linked or circularized by a nucleotide or non-nucleotide linker as described herein, wherein the oligonucleotide does not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotide. Applicant has surprisingly found that the presense of ribonucleotides (e.g., nucleotides having a 2'-hydroxyl group) within the siNA molecule is not required or essential to support RNAi activity. As such, in one embodiment, all positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA polynucleotide that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the single stranded polynucleotide has complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the single stranded siNA molecule of the invention comprises about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system comprising a single stranded polynucleotide having complementarity to a target nucleic acid sequence, wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The siNA optionally further comprises about 1 to about 4 or more (e.g., about 1, 2, 3, 4 or more) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group. In any of these embodiments, any purine nucleotides present in the antisense region are alternatively 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA (i.e., purine nucleotides present in the sense and/or antisense region) can alternatively be locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine nucleotides are LNA nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA are alternatively 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides). In another embodiment, any modified nucleotides present in the single stranded siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As

such, chemically modified nucleotides present in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

5 In one embodiment, the invention features a method for modulating the expression of a HCV gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the HCV gene in the cell.

10 In one embodiment, the invention features a method for modulating the expression of a HCV gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the  
15 sequence of the target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the HCV gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one HCV gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA  
20 strands comprises a sequence complementary to RNA of the HCV genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the HCV genes in the cell.

In another embodiment, the invention features a method for modulating the expression of two or more HCV genes within a cell comprising: (a) synthesizing one or  
25 more siNA molecules of the invention, which can be chemically-modified, wherein the siNA strands comprise sequences complementary to RNA of the HCV genes and wherein the sense strand sequences of the siNAs comprise sequences identical or substantially similar to the sequences of the target RNAs; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the HCV  
30 genes in the cell.



In another embodiment, the invention features a method for modulating the expression of more than one HCV gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene and  
5 wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequences of the target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the HCV genes in the cell.

In one embodiment, the invention features a method of modulating the expression  
10 of a HCV gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the HCV gene in the tissue explant. In  
15 another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the HCV gene in that organism.

In one embodiment, the invention features a method of modulating the expression of a HCV gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the  
20 invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate  
25 the expression of the HCV gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the HCV gene in that organism.

In another embodiment, the invention features a method of modulating the  
30 expression of more than one HCV gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV genes; and (b)

introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the HCV genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the HCV genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a HCV gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the HCV gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one HCV gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the HCV genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the HCV genes in the organism.

In one embodiment, the invention features a method for modulating the expression of a HCV gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the HCV gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one HCV gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene; and (b) contacting a cell in vitro or in vivo with the siNA molecule under conditions suitable to modulate the expression of the HCV genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a HCV gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene; and (b) contacting  
5 the siNA molecule with a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the HCV gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the HCV gene in that organism.

10 In another embodiment, the invention features a method of modulating the expression of more than one HCV gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a  
15 particular organism under conditions suitable to modulate the expression of the HCV genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the HCV genes in that organism.

20 In one embodiment, the invention features a method of modulating the expression of a HCV gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate  
25 the expression of the HCV gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one HCV gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the HCV gene;  
30 and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the HCV genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a HCV gene in an organism comprising contacting the organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the HCV gene in the organism.

- 5 In another embodiment, the invention features a method of modulating the expression of more than one HCV gene in an organism comprising contacting the organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the HCV genes in the organism.

The siNA molecules of the invention can be designed to inhibit, down regulate or target (HCV) gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If  
10 alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms.  
15 Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications,  
20 molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target  
30 conserved sequences corresponding to a gene family or gene families such as HCV family genes. As such, siNA molecules targeting multiple HCV targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of

gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, the progression and/or maintenance of HCV infection, liver failure, hepatocellular carcinoma, cirrhosis and other indications that can respond to the level of HCV in a cell or tissue.

10 In one embodiment, siNA molecule(s) and/or methods of the invention are used to inhibit or down regulate the expression of gene(s) that encode RNA referred to by Genbank Accession, for example HCV genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example Genbank Accession Nos. shown in **Table I.**

15 In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

30 In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of  $4^N$ , where N represents the number of base paired nucleotides in each of the siNA construct



strands (eg. for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be  $4^{19}$ ); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target HCV RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 6 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of HCV RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target HCV RNA sequence. The target HCV RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a method for diagnosing a disease or condition in a subject comprising administering to the subject a composition of the invention under conditions suitable for the diagnosis of the disease or condition in the subject. In another embodiment, the invention features a method for treating or preventing a disease or condition in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other therapeutic compounds.

In another embodiment, the invention features a method for validating a HCV gene target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of a HCV target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the HCV target gene in the cell, tissue, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

In another embodiment, the invention features a method for validating a HCV gene target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence

complementary to RNA of a HCV target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the HCV target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

5 By "biological system" is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human, animal, plant, insect, bacterial, viral or other sources, wherein the system comprises the components required for RNAi activity. The term "biological system" includes, for example, a cell, tissue, or organism, or extract thereof. The term biological system also includes reconstituted RNAi systems  
10 that can be used in an *in vitro* setting.

By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or  
15 chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

In one embodiment, the invention features a kit containing a siNA molecule of the  
20 invention, which can be chemically-modified, that can be used to modulate the expression of a HCV target gene in a biological system, including, for example, in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one HCV target gene in a biological  
25 system, including, for example, in a cell, tissue, or organism.

In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

30 In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the

siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the  
5 siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second  
10 oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a  
15 stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support  
20 such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place  
25 concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic  
30 conditions.

In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are

synthesized in tandem using a cleavable linker attached to the first sequence which acts a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

5           In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first  
10   sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety than can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length  
15   sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c)  
20   above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise  
25   similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

30           In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is



complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the  
5 deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

In another embodiment, the method of synthesis of siNA molecules of the  
10 invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of Formulae  
15 I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b)  
20 assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and  
25 antisense strands of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of  
30 step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

5 In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

10 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand  
15 of the siNA molecule and a complementary target RNA sequence.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA  
20 molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical  
25 modifications described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase  
30 capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having

any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the  
5 chemically-modified siNA molecule.

In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against a HCV in a cell, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would  
10 decrease the efficacy of RNAi mediated by such siNA constructs.

In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against HCV comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for  
15 isolating siNA molecules having improved RNAi activity.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a HCV target RNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable  
20 for isolating siNA molecules having improved RNAi activity against the target RNA.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a HCV target DNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable  
25 for isolating siNA molecules having improved RNAi activity against the target DNA.

In one embodiment, the invention features siNA constructs that mediate RNAi against a HCV, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct.

In another embodiment, the invention features a method for generating siNA  
30 molecules against HCV with improved cellular uptake comprising (a) introducing

nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

In one embodiment, the invention features siNA constructs that mediate RNAi  
5 against a HCV, wherein the siNA construct comprises one or more chemical  
modifications described herein that increases the bioavailability of the siNA construct,  
for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent  
conjugates that improve the pharmacokinetics of the siNA construct, or by attaching  
conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples  
10 of such conjugates are described in Vargeese *et al.*, U.S. Serial No. 10/201,394  
incorporated by reference herein.

In one embodiment, the invention features a method for generating siNA  
molecules of the invention with improved bioavailability, comprising (a) introducing a  
conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of  
15 step (a) under conditions suitable for isolating siNA molecules having improved  
bioavailability. Such conjugates can include ligands for cellular receptors, such as  
peptides derived from naturally occurring protein ligands; protein localization sequences,  
including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and  
other co-factors, such as folate and N-acetylgalactosamine; polymers, such as  
20 polyethyleneglycol (PEG); phospholipids; cholesterol; polyamines, such as spermine or  
spermidine; and others.

In another embodiment, the invention features a method for generating siNA  
molecules of the invention with improved bioavailability comprising (a) introducing an  
excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a)  
25 under conditions suitable for isolating siNA molecules having improved bioavailability.  
Such excipients include polymers such as cyclodextrins, lipids, cationic lipids,  
polyamines, phospholipids, nanoparticles, receptors, ligands, and others.

The term "ligand" refers to any compound or molecule, such as a drug, peptide,  
hormone, or neurotransmitter, that is capable of interacting with another compound, such  
30 as a receptor, either directly or indirectly. The receptor that interacts with a ligand can be  
present on the surface of a cell or can alternately be an intercellular receptor. Interaction

of the ligand with the receptor can result in a biochemical reaction, or can simply be a physical interaction or association.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing  
5 nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular  
10 weight, preferably from about 2,000 to about 50,000 daltons (Da).

The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include a siNA molecule of the invention and a vehicle that promotes introduction of the siNA into  
15 cells of interest as described herein (e.g., using lipids and other methods of transfection known in the art, see for example Beigelman *et al.*, US 6,395,713). The kit can be used for target validation, such as in determining gene function and/or activity, or in drug optimization, and in drug discovery (see for example Usman *et al.*, USSN 60/402,996). Such a kit can also include instructions to allow a user of the kit to practice the invention.

20 The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication, for example by mediating RNA interference "RNAi" or  
25 gene silencing in a sequence-specific manner; see for example Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.*, 2001, *Nature*, 411, 494-498; and Kreutzer *et al.*, International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.*, International PCT Publication No. WO 00/01846; Mello and Fire,  
30 International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.*, International PCT Publication No. WO



00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002, *Science*, 297, 2056-60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non limiting examples of siNA molecules of the invention are shown in **Figures 4-6**, and **Tables II, III, and IV** herein. For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 19 base pairs); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo* or *in vitro* to generate an active siNA molecule capable of

mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell.*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiment, the siNA molecule of the invention comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linkers molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der waals interactions, hydrophobic interactions, and/or stacking interactions. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering

oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237).

By “asymmetric hairpin” as used herein is meant a linear siNA molecule comprising an antisense region, a loop portion that can comprise nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g., about 19, 20, 21, or 22) nucleotides) and a loop region comprising about 4 to about 8 (e.g., about 4, 5, 6, 7, or 8) nucleotides, and a sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region. The asymmetric hairpin siNA molecule can also comprise a 5'-terminal phosphate group that can be chemically modified. The loop portion of the asymmetric hairpin siNA molecule can comprise nucleotides, non-nucleotides, linker molecules, or conjugate molecules as described herein.

By “asymmetric duplex” as used herein is meant a siNA molecule having two separate strands comprising a sense region and an antisense region, wherein the sense region comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex. For example, an asymmetric duplex siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g. about 19, 20, 21, or 22) nucleotides) and a

sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region.

By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

By "inhibit", "down-regulate", or "reduce", it is meant that the expression of a gene, or level of RNA molecules or equivalent RNA molecules encoding one or more gene products, or activity of one or more gene products, is reduced below that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In one embodiment, inhibition, down-regulation or reduction with an siNA molecule is below that level observed in the presence of an inactive or attenuated molecule that is unable to mediate an RNAi response. In another embodiment, inhibition, down-regulation, or reduction with a siNA molecule is below that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment, inhibition, down-regulation, or reduction of gene expression with a siNA molecule of the instant invention is greater in the presence of the siNA molecule than in its absence.

By "gene" or "target gene" is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts.

By "HCV" as used herein is meant the hepatitis C Virus or any protein, peptide, or polypeptide, having hepatitis C virus activity or encoded by the HCV genome. The term

“HCV” also includes nucleic acid molecules encoding RNA or protein(s) associated with the development and/or maintenance of HCV infection, such as nucleic acid molecules which encode HCV RNA or polypeptides (such as polynucleotides having Genbank Accession numbers shown in Table I), including polypeptides of different strains of HCV, mutant HCV genes, and splice variants of HCV genes, as well as genes involved in HCV pathways of gene expression and/or HCV activity. Also, the term “HCV” is meant to encompass HCV viral gene products and genes that modulate cellular targets for HCV infection, such as those described herein.

By "HCV protein" is meant, protein, peptide, or polypeptide, having hepatitis C virus activity or encoded by the HCV genome.

By "highly conserved sequence region" is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

By “sense region” is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By “antisense region” is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

By “target nucleic acid” is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.*, 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*,



1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, or 10 nucleotides out of a total of 10 nucleotides in the first oligonucleotide being based paired to a second nucleic acid sequence having 10 nucleotides represents 50%, 60%, 70%, 80%, 90%, and 100% complementary respectively). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

10 The siNA molecules of the invention represent a novel therapeutic approach to treat various diseases and conditions, including HCV infection, liver failure, hepatocellular carcinoma, cirrhosis and any other indications that can respond to the level of HCV in a cell or tissue.

In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to about 23 base pairs (e.g., about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (e.g., about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (e.g., 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (e.g., about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Table II**. Exemplary synthetic siNA molecules of the invention are shown in **Tables III and IV** and/or **Figures 4-5**.

25 As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell can be present in an organism, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables II-III** and/or **Figures 4-5**. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

10 In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a  $\beta$ -D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

25 By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells.

The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term

phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

The term "phosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise an acetyl or protected acetyl group.

- 5       The term "thiophosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z comprises an acetyl or protected acetyl group and W comprises a sulfur atom or alternately W comprises an acetyl or protected acetyl group and Z comprises a sulfur atom.

- 10       The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

- 15       The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

- 20       The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein, e.g., a siRNA molecule of the invention can be adapted for use to treat for example HCV infection, liver failure, hepatocellular carcinoma, cirrhosis and other indications that can respond to the level of HCV in a cell or tissue. For example, to treat a particular disease or condition, the siNA molecules can be administered to a subject or can be administered to other appropriate cells evident to those skilled in the art, 25 individually or in combination with one or more drugs under conditions suitable for the treatment.

- 30       In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules can be used in combination with one or more known therapeutic agents to treat a disease or condition. Non-limiting examples of other therapeutic agents

that can be readily combined with a siNA molecule of the invention are enzymatic nucleic acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and other organic and/or inorganic compounds including metals, salts and ions.

5        In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-  
10        complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

15        In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

20        In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from  
25        transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that  
30        provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate

gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

## **BRIEF DESCRIPTION OF THE DRAWINGS**

**Figure 1** shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

**Figure 2** shows a MALDI-TOF mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

**Figure 3** shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by



RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms  
 5 which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

**Figure 4A-F** shows non-limiting examples of chemically-modified siNA  
 10 constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N). Various modifications are shown for the sense and antisense strands of the siNA constructs.

**Figure 4A:** The sense strand comprises 21 nucleotides wherein the two terminal  
 15 3'-nucleotides are optionally base paired and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the  
 20 target RNA sequence, and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s" connects the (N N) nucleotides  
 25 in the antisense strand.

**Figure 4B:** The sense strand comprises 21 nucleotides wherein the two terminal  
 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can  
 30 comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-

nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the sense and antisense strand.

**Figure 4C:** The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'- terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand.

**Figure 4D:** The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise

ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand.

5        **Figure 4E:** The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

10    The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise

15    ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand.

20        **Figure 4F:** The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The

25    antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy

30    nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or

other modified internucleotide linkage as described herein, shown as “s” connects the (N N) nucleotides in the antisense strand. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of the invention. Furthermore, when a glyceryl moiety (L) is present at the 3'-end of the antisense strand  
 5 for any construct shown in Figure 4 A-F, the modified internucleotide linkage is optional.

**Figure 5A-F** shows non-limiting examples of specific chemically-modified siNA sequences of the invention. **A-F** applies the chemical modifications described in **Figure 4A-F** to a HCV siNA sequence.

10 **Figure 6** shows non-limiting examples of different siNA constructs of the invention. The examples shown (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides.  
 15 Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 *in vivo* and/or *in vitro*. In another example, construct 3 can be used to generate construct 2 under the  
 20 same principle wherein a linker is used to generate the active siNA construct 2 *in vivo* and/or *in vitro*, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 *in vivo* and/or *in vitro*. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use *in vivo* or *in vitro* and/or *in vitro*.

25 **Figure 7A-C** is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate siNA hairpin constructs.

**Figure 7A:** A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined HCV target sequence, wherein the sense region comprises, for example,  
 30 about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

**Figure 7B:** The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a HCV target sequence and having self-complementary sense and antisense regions.

5        **Figure 7C:** The construct is heated (for example to about 95°C) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed  
10 such that a 3'-terminal nucleotide overhang results from the transcription, for example by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul *et al.*, 2002, *Nature Biotechnology*, 29, 505-508.

**Figure 8A-C** is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

15        **Figure 8A:** A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined HCV target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined sequence (X).

20        **Figure 8B:** The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

25        **Figure 8C:** The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector for expression in cells. The transcription cassette is designed such that a U6 promoter region flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

**Figure 9A-E** is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as messenger RNA.



**Figure 9A:** A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA.

5        **Figure 9B&C:** (**Figure 9B**) The sequences are pooled and are inserted into vectors such that (**Figure 9C**) transfection of a vector into cells results in the expression of the siNA.

**Figure 9D:** Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

10       **Figure 9E:** The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

**Figure 10** shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3'-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5'-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

**Figure 11** shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-modifications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example, in a cell culture system such as a

luciferase reporter assay. Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

5        **Figure 12** shows a non-limiting example of siRNA constructs 29579/ 29586 and 29578/ 29585 targeting viral replication of an HCV/poliovirus chimera in comparison to an inverse siNA control construct 29593/29600.

10        **Figure 13** shows a non-limiting example of a dose response study of a siRNA construct 29579/ 29586 targeting viral replication of an HCV/poliovirus chimera in comparison to an inverse siNA control construct 29593/ 29600. The inhibition of HCV/poliovirus chimera replication by 29579/ 29586 siNA construct was measured at 1 nM, 5 nM, 10 nM, and 25 nM concentrations of 29579/ 29586 siNA construct.

15        **Figure 14** shows a non-limiting example of a chemically modified siRNA construct 30051/30053 targeting viral replication of an HCV/poliovirus chimera in comparison to an inverse siNA control construct 30052/ 30054.

**Figure 15** shows a non-limiting example of a chemically modified siRNA construct 30055/ 30057 targeting viral replication of an HCV/poliovirus chimera in comparison to an inverse siNA control construct 30056/ 30058.

20        **Figure 16** shows a non-limiting example of several chemically modified siRNA constructs targeting viral replication of an HCV/poliovirus chimera at 10 nM treatment in comparison to a lipid control and an inverse siNA control construct 29593/ 29600.

**Figure 17** shows a non-limiting example of several chemically modified siRNA constructs targeting viral replication of a HCV/poliovirus chimera at 25 nM treatment in comparison to a lipid control and an inverse siNA control construct 29593/ 29600.

25        **Figure 18** shows a non-limiting example of several chemically modified siRNA constructs targeting viral replication of a Huh7 HCV replicon system at 25 nM treatment in comparison to untreated cells (“cells”), cells transfected with lipofectamine (“LFA2K”) and inverse siNA control constructs.

**Figure 19** shows a non-limiting example of a dose response study using chemically modified siNA molecules (Stab 4/5, see **Table IV**) targeting HCV RNA sites 291, 300, and 303 in a Huh7 HCV replicon system at 5, 10, 25, and 100 nM treatment in comparison to untreated cells ("cells"), cells transfected with lipofectamine ("LFA") and  
5 inverse siNA control constructs.

**Figure 20** shows a non-limiting example of several chemically modified siNA constructs (Stab 7/8, see **Table IV**) targeting viral replication in a Huh7 HCV replicon system at 25 nM treatment in comparison to untreated cells ("cells"), cells transfected with lipofectamine ("Lipid") and inverse siNA control constructs.

10 **Figure 21** shows a non-limiting example of a dose response study using chemically modified siNA molecules (Stab 7/8, see **Table IV**) targeting HCV site 327 in a Huh7 HCV replicon system at 5, 10, 25, 50, and 100 nM treatment in comparison to inverse siNA control constructs.

15 **Figure 22** shows the results of a study in which siNA/interferon combination treatments were assayed using 0-100 nM siNA in a HCV Subgenomic Replicon system in Huh7 cells compared to interferon alone.

**Figure 23** shows non-limiting examples of phosphorylated siNA molecules of the invention, including linear and duplex constructs and asymmetric derivatives thereof.

20 **Figure 24** shows non-limiting examples of chemically modified terminal phosphate groups of the invention.

## DETAILED DESCRIPTION OF THE INVENTION

### Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant  
25 to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or

“improved RNAi activity” is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA  
 5 or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*,  
 10 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999,  
 15 *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a  
 20 mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III  
 25 enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal  
 30 RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an

RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can  
 5 also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237). As such, siNA  
 10 molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806,  
 15 were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human  
 20 embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands  
 25 with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-  
 30 end (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309); however, siRNA molecules lacking a 5'-



phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

### Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.*, International PCT Publication No. WO 99/54459, Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.*, 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2  $\mu$ mol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 second coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2  $\mu$ mol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60  $\mu$ L of 0.11 M = 6.6  $\mu$ mol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60  $\mu$ L of 0.25 M = 15  $\mu$ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40  $\mu$ L of 0.11 M = 4.4  $\mu$ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40

5  $\mu\text{L}$  of 0.25 M = 10  $\mu\text{mol}$ ) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM  $\text{I}_2$ , 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

15 Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aqueous methylamine (1 mL) at 65 °C for 10 minutes. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H<sub>2</sub>O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants,
 20 containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and
 25 makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2  $\mu\text{mol}$  scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides.
 30 **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2  $\mu\text{mol}$  scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal

modification to the cycle. A 33-fold excess (60  $\mu$ L of 0.11 M = 6.6  $\mu$ mol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60  $\mu$ L of 0.25 M = 15  $\mu$ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120  $\mu$ L of 0.11 M = 13.2  $\mu$ mol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120  $\mu$ L of 0.25 M = 30  $\mu$ mol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I<sub>2</sub>, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 minutes. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H<sub>2</sub>O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300  $\mu$ L of a solution of 1.5 mL *N*-methylpyrrolidinone, 750  $\mu$ L TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH<sub>4</sub>HCO<sub>3</sub>.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 minutes. The vial is brought to room temperature TEA•3HF (0.1 mL) is added and the vial is

heated at 65 °C for 15 minutes. The sample is cooled at -20 °C and then quenched with 1.5 M  $\text{NH}_4\text{HCO}_3$ .

For purification of the trityl-on oligomers, the quenched  $\text{NH}_4\text{HCO}_3$  solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 minutes. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.*, 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.*, 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as described herein can also be readily adapted to large-scale synthesis platforms employing batch reactors, synthesis columns and the like.

A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

The nucleic acid molecules of the present invention can be modified extensively to  
5 enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*, the totality of which is  
10 hereby incorporated herein by reference) and re-suspended in water.

In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus.  
15 The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

#### Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar  
20 and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken *et al.*, 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication  
25 No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.*, U.S. Pat. No. 6,300,074; and Burgin *et al.*, *supra*; all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid  
30 molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.



There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with

5 nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS*, 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein *et al.*, *International Publication* PCT No.

10 WO 92/07065; Perrault *et al.* *Nature*, 1990, 344, 565-568; Pieken *et al.* *Science*, 1991, 253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman *et al.* *International Publication* PCT No. WO 93/15187; Sproat, *U.S. Pat.* No. 5,334,711 and Beigelman *et al.*, 1995, *J. Biol. Chem.*, 270, 25702; Beigelman *et al.*, *International PCT publication* No. WO 97/26270; Beigelman *et al.*, *U.S. Pat.* No.

15 5,716,824; Usman *et al.*, *U.S. Pat.* No. 5,627,053; Woolf *et al.*, *International PCT Publication* No. WO 98/13526; Thompson *et al.*, *USSN* 60/082,404 which was filed on April 20, 1998; Karpeisky *et al.*, 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010;

20 all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify

25 the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi in cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity.

30 Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

In one embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.*, International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the

invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, phospholipids, cholesterol, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example  
5 proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues,  
10 in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

The term "biodegradable linker" as used herein, refers to a nucleic acid or non-  
15 nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability  
20 of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer  
25 nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

30 The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include

5 therapeutically active molecules such as antibodies, cholesterol, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention

10 also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a

15 phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

Therapeutic nucleic acid molecules (*e.g.*, siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid

20 molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

25 In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

Use of the nucleic acid-based molecules of the invention will lead to better

30 treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple siNA molecules targeted to different genes; nucleic acid molecules

coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid  
 5 molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'-cap structure, for example on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

10 By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-  
 15 terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap includes, but is not limited to glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuransyl nucleotide;  
 20 acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging  
 25 methylphosphonate moiety.

In non-limiting examples, the 3'-cap includes, but is not limited to glyceryl, inverted deoxy abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl  
 30 phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-



dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging  
 5 methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to  
 10 exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12  
 15 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO<sub>2</sub> or N(CH<sub>3</sub>)<sub>2</sub>, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain,  
 20 branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO<sub>2</sub>, halogen, N(CH<sub>3</sub>)<sub>2</sub>, amino, or SH. The term "alkyl" also includes alkynyl groups that have an  
 25 unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O,  
 30 =S, NO<sub>2</sub> or N(CH<sub>3</sub>)<sub>2</sub>, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090;

Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate, carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417, and Mesmaeker *et al.*, 1994, *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.*, U.S. Pat. No. 5,998,203.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of  $\beta$ -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH<sub>2</sub> or 2'-O- NH<sub>2</sub>, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro*, stability, and ease of introduction of such oligonucleotides to the target site, *e.g.*, to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

### Administration of Nucleic Acid Molecules

A siRNA molecule of the invention can be adapted for use to treat for example HCV infection, liver failure, hepatocellular carcinoma, cirrhosis and other indications that can respond to the level of HCV in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer *et al.*, 1999, *Mol. Membr. Biol.*, 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee *et al.*, 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.*, U.S. Pat. No. 6,395,713 and Sullivan *et al.*, PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as biodegradable polymers, hydrogels, cyclodextrins (see for example Gonzalez *et al.*, 1999, *Bioconjugate Chem.*, 10, 1068-1074; Wang *et al.*, International PCT publication Nos. WO 03/47518 and WO 03/46185), poly(lactic-co-glycolic)acid (PLGA) and PLCA microspheres (see for example US Patent 6,447,796 and US Patent Application Publication No. US 2002130430), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can take place using standard needle and syringe methodologies, or by needle-free technologies such as those described in Conry *et al.*, 1999, *Clin. Cancer Res.*, 5, 2330-2337 and Barry *et al.*, International PCT Publication No. WO 99/31262. The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

In one embodiment, a siNA molecule of the invention is complexed with membrane disruptive agents such as those described in U.S. Patent Application Publication No. 20010007666, incorporated by reference herein in its entirety including the drawings. In another embodiment, the membrane disruptive agent or agents and the  
5 siNA molecule are also complexed with a cationic lipid or helper lipid molecule, such as those lipids described in U.S. Patent No. 6,235,310, incorporated by reference herein in its entirety including the drawings.

Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and  
10 the like. The polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as  
15 tablets, capsules or elixirs for oral administration, suppositories for rectal administration, sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds,  
20 *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or subject, including for example a human. Suitable forms, in part, depend upon the  
25 use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that  
30 prevent the composition or formulation from exerting its effect.



By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess HCV.

By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Joliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF *et al*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists  
 5 opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al.* *Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al.*, *Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized  
 10 target tissues (Lasic *et al.*, *Science* 1995, 267, 1275-1276; Oku *et al.*, 1995, *Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al.*, *J. Biol. Chem.* 1995, 270, 24864-24870; Choi *et al.*, International PCT  
 15 Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

20 The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R.  
 25 Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the  
 30 occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the

physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

5       The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (*e.g.*, intravenous), intramuscular, or  
10   intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active  
15   ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

      Compositions intended for oral use can be prepared according to any method  
20   known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets.  
25   These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known  
30   techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained

action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is  
5 mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-  
10 methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products  
15 of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring  
20 agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for  
25 example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a  
30 dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already

mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either



be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 5 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular subject depends upon 10 a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the 15 animal feed or drinking water. It can be convenient to formulate the animal feed and drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a 20 subject in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For 25 example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomuroid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly 30 depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biatennary or monoantennary

chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly *et al.*, 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.*, 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese *et al.*, USSN 10/201,394, filed August 13, 2001; and Matulic-Adamic *et al.*, USSN 10/151,116, filed May 17, 2002. In one embodiment, nucleic acid molecules of the invention are complexed with or covalently attached to nanoparticles, such as Hepatitis B virus S, M, or L envelope proteins (see for example Yamado *et al.*, 2003, *Nature Biotechnology*, 21, 885).

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (*e.g.*, Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J. Virol.*, 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science*, 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol. Chem.*, 269, 25856).

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); and c) a nucleic acid sequence encoding at least one of the siNA molecules of the instant invention; wherein said sequence is operably linked to said initiation region and said termination region, in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein

operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the invention; and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber *et al.*, 1993, *Methods Enzymol.*, 217, 47-66; Zhou *et al.*, 1990, *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.*, 1993, *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992, *EMBO J.*, 11, 4411-8; Lisiewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A*, 90, 8000-4; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson *et al.*, *supra*; Couture and Stinchcomb, 1996, *supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, U.S. Pat. No. 5,624,803; Good *et al.*, 1997, *Gene Ther.*, 4, 45; Beigelman *et al.*, International PCT Publication No. WO 96/18736). The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, *supra*).

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one

embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

5        In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the  
10        termination region in a manner that allows expression and/or delivery of the siNA molecule.

         In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked  
15        to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

         In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule,  
20        wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

#### HCV biology and biochemistry

25        In 1989, the Hepatitis C Virus (HCV) was determined to be an RNA virus and was identified as the causative agent of most non-A non-B viral Hepatitis (Choo *et al.*, 1989, *Science*, 244, 359-362). Unlike retroviruses such as HIV, HCV does not go through a DNA replication phase and no integrated forms of the viral genome into the host chromosome have been detected (Houghton *et al.*, 1991, *Hepatology*, 14, 381-388).  
30        Rather, replication of the coding (plus) strand is mediated by the production of a replicative (minus) strand leading to the generation of several copies of plus strand HCV



RNA. The genome consists of a single, large, open-reading frame that is translated into a polyprotein (Kato *et al.*, 1991, *FEBS Letters*, 280: 325-328). This polyprotein subsequently undergoes post-translational cleavage, producing several viral proteins (Leinbach *et al.*, 1994, *Virology*, 204:163-169).

5        Examination of the 9.5-kilobase genome of HCV has demonstrated that the viral nucleic acid can mutate at a high rate (Smith *et al.*, 1997 *Mol. Evol.* 45, 238-246). This rate of mutation has led to the evolution of several distinct genotypes of HCV that share approximately 70% sequence identity (Simmonds *et al.*, 1994, *J. Gen. Virol.* 75, 1053-1061). It is important to note that these sequences are evolutionarily quite distant. For  
10        example, the genetic identity between humans and primates such as the chimpanzee is approximately 98%. In addition, it has been demonstrated that an HCV infection in an individual patient is composed of several distinct and evolving quasispecies that have 98% identity at the RNA level. Thus, the HCV genome is hypervariable and continuously changing. Although the HCV genome is hypervariable, there are 3 regions  
15        of the genome that are highly conserved. These conserved sequences occur in the 5' and 3' non-coding regions as well as the 5'-end of the core protein coding region and are thought to be vital for HCV RNA replication as well as translation of the HCV polyprotein. Thus, therapeutic agents that target these conserved HCV genomic regions may have a significant impact over a wide range of HCV genotypes. Moreover, it is  
20        unlikely that drug resistance will occur with enzymatic nucleic acids specific to conserved regions of the HCV genome. In contrast, therapeutic modalities that target inhibition of enzymes such as the viral proteases or helicase are likely to result in the selection for drug resistant strains since the RNA for these viral encoded enzymes is located in the hypervariable portion of the HCV genome.

25        After initial exposure to HCV, a patient experiences a transient rise in liver enzymes, which indicates that inflammatory processes are occurring (Alter *et al.*, IN: Seeff LB, Lewis JH, eds. *Current Perspectives in Hepatology*. New York: Plenum Medical Book Co; 1989:83-89). This elevation in liver enzymes occurs at least 4 weeks after the initial exposure and may last for up to two months (Farci *et al.*, 1991, *New*  
30        *England Journal of Medicine*. 325, 98-104). Prior to the rise in liver enzymes, it is possible to detect HCV RNA in the patient's serum using RT-PCR analysis (Takahashi *et al.*, 1993, *American Journal of Gastroenterology*. 88, 240-243). This stage of the disease

is called the acute stage and usually goes undetected since 75% of patients with acute viral hepatitis from HCV infection are asymptomatic. The remaining 25% of these patients develop jaundice or other symptoms of hepatitis.

Although acute HCV infection is a benign disease, as many as 80% of acute HCV patients progress to chronic liver disease as evidenced by persistent elevation of serum alanine aminotransferase (ALT) levels and by continual presence of circulating HCV RNA (Sherlock, 1992, *Lancet*, 339, 802). The natural progression of chronic HCV infection over a 10 to 20 year period leads to cirrhosis in 20 to 50% of patients (Davis *et al.*, 1993, *Infectious Agents and Disease*, 2, 150, 154) and progression of HCV infection to hepatocellular carcinoma has been well documented (Liang *et al.*, 1993, *Hepatology*. 18, 1326-1333; Tong *et al.*, 1994, *Western Journal of Medicine*, 160, 133-138). There have been no studies that have determined sub-populations that are most likely to progress to cirrhosis and/or hepatocellular carcinoma, thus all patients have equal risk of progression.

It is important to note that the survival for patients diagnosed with hepatocellular carcinoma is only 0.9 to 12.8 months from initial diagnosis (Takahashi *et al.*, 1993, *American Journal of Gastroenterology*. 88, 240-243). Treatment of hepatocellular carcinoma with chemotherapeutic agents has not proven effective and only 10% of patients will benefit from surgery due to extensive tumor invasion of the liver (Trinchet *et al.*, 1994, *Presse Medicin*. 23, 831-833). Given the aggressive nature of primary hepatocellular carcinoma, the only viable treatment alternative to surgery is liver transplantation (Pichlmayr *et al.*, 1994, *Hepatology*. 20, 33S-40S).

Upon progression to cirrhosis, patients with chronic HCV infection present with clinical features, which are common to clinical cirrhosis regardless of the initial cause (D'Amico *et al.*, 1986, *Digestive Diseases and Sciences*. 31, 468-475). These clinical features may include: bleeding esophageal varices, ascites, jaundice, and encephalopathy (Zakim D, Boyer TD. *Hepatology a textbook of liver disease*. Second Edition Volume 1. 1990 W.B. Saunders Company. Philadelphia). In the early stages of cirrhosis, patients are classified as compensated, the stage at which the patient's liver is still able to detoxify metabolites in the blood-stream although liver tissue damage has occurred. In addition, most patients with compensated liver disease are asymptomatic and the minority with symptoms report only minor symptoms, such as dyspepsia and weakness. In the later

stages of cirrhosis, patients are classified as decompensated, the stage at which the ability of the liver to detoxify metabolites in the bloodstream is diminished. It is at the decompensated stage that the clinical features described above present.

In 1986, D'Amico *et al.* described the clinical manifestations and survival rates in 1155 patients with both alcoholic and viral associated cirrhosis (D'Amico *supra*). Of the 1155 patients, 435 (37%) had compensated disease although 70% were asymptomatic at the beginning of the study. The remaining 720 patients (63%) had decompensated liver disease with 78% presenting with a history of ascites, 31% with jaundice, 17% had bleeding and 16% had encephalopathy. Hepatocellular carcinoma was observed in six (.5%) patients with compensated disease and in 30 (2.6%) patients with decompensated disease.

Over the course of six years, the patients with compensated cirrhosis developed clinical features of decompensated disease at a rate of 10% per year. In most cases, ascites was the first presentation of decompensation. In addition, hepatocellular carcinoma developed in 59 patients who initially presented with compensated disease by the end of the six-year study.

With respect to survival, the D'Amico study indicated that the five-year survival rate for all patients in the study was only 40%. The six-year survival rate for the patients who initially had compensated cirrhosis was 54% while the six-year survival rate for patients who initially presented with decompensated disease was only 21%. There were no significant differences in the survival rates between the patients who had alcoholic cirrhosis and the patients with viral related cirrhosis. The major causes of death for the patients in the D'Amico study were liver failure in 49%; hepatocellular carcinoma in 22%; and bleeding in 13% (D'Amico *supra*).

Chronic Hepatitis C is a slowly progressing inflammatory disease of the liver, mediated by a virus (HCV) that can lead to cirrhosis, liver failure and/or hepatocellular carcinoma over a period of 10 to 20 years. In the US, it is estimated that infection with HCV accounts for 50,000 new cases of acute hepatitis in the United States each year (NIH Consensus Development Conference Statement on Management of Hepatitis C March 1997). The prevalence of HCV in the United States is estimated at 1.8% and the CDC places the number of chronically infected Americans at approximately 4.5 million

people. The CDC also estimates that up to 10,000 deaths per year are caused by chronic HCV infection.

Numerous well controlled clinical trials using interferon (IFN-alpha) in the treatment of chronic HCV infection have demonstrated that treatment three times a week results in lowering of serum ALT values in approximately 50% (40% - 70%) of patients by the end of 6 months of therapy (Davis *et al.*, 1989, *New England Journal of Medicine*, 321, 1501-1506; Marcellin *et al.*, 1991, *Hepatology*, 13, 393-397; Tong *et al.*, 1997, *Hepatology*, 26, 747-754; Tong *et al.*, 1997, *Hepatology*, 26, 1640-1645). However, following cessation of interferon treatment, approximately 50% of the responding patients relapsed, resulting in a "durable" response rate as assessed by normalization of serum ALT concentrations of approximately 20 - 25%.

Direct measurement of HCV RNA is possible through use of either the branched-DNA or Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) analysis. In general, RT-PCR methodology is more sensitive and leads to a more accurate assessment of the clinical course (Tong *et al.*, *supra*). Studies that have examined six months of type 1 interferon therapy using changes in HCV RNA values as a clinical endpoint have demonstrated that up to 35% of patients have a loss of HCV RNA by the end of therapy (Marcellin *et al.*, *supra*). However, as with the ALT endpoint, about 50% of the patients relapse within six months following cessation of therapy, resulting in a durable virologic response of only 12% (Marcellin *et al.*, *supra*). Studies that have examined 48 weeks of therapy have demonstrated that the sustained virological response is up to 25% (NIH consensus statement: 1997). Thus, standard of care for treatment of chronic HCV infection with type 1 interferon is now 48 weeks of therapy using changes in HCV RNA concentrations as the primary assessment of efficacy (Hoofnagle *et al.*, 1997, *New England Journal of Medicine*, 336, 347-356).

Side effects resulting from treatment with type 1 interferons can be divided into four general categories, which include: (1) Influenza-like symptoms; (2) Neuropsychiatric; (3) Laboratory abnormalities; and (4) Miscellaneous (Dusheiko *et al.*, 1994, *Journal of Viral Hepatitis*, 1, 3-5). Examples of influenza-like symptoms include fatigue, fever, myalgia, malaise, appetite loss, tachycardia, rigors, headache, and arthralgias. The influenza-like symptoms are usually short-lived and tend to abate after the first four weeks of dosing (Dushieko *et al.*, *supra*). Neuropsychiatric side effects

include irritability, apathy, mood changes, insomnia, cognitive changes, and depression. The most important of these neuropsychiatric side effects is depression and patients who have a history of depression should not be given type 1 interferon. Laboratory abnormalities include reduction in myeloid cells, including granulocytes, platelets and to  
 5 a lesser extent red blood cells. These changes in blood cell counts rarely lead to any significant clinical sequelae (Dushieko *et al.*, *supra*). In addition, increases in triglyceride concentrations and elevations in serum alanine and aspartate aminotransferase concentration have been observed. Finally, thyroid abnormalities have been reported. These thyroid abnormalities are usually reversible after cessation of  
 10 interferon therapy and can be controlled with appropriate medication while on therapy. Miscellaneous side effects include nausea, diarrhea, abdominal and back pain, pruritus, alopecia, and rhinorrhea. In general, most side effects will abate after 4 to 8 weeks of therapy (Dushieko *et al.*, *supra*).

The use of small interfering nucleic acid molecules targeting HCV genes therefore  
 15 provides a class of novel therapeutic agents that can be used in the treatment and diagnosis of HCV infection, liver failure, hepatocellular carcinoma, cirrhosis or any other disease or condition that responds to modulation of HCV genes.

#### Examples:

The following are non-limiting examples showing the selection, isolation,  
 20 synthesis and activity of nucleic acids of the instant invention.

#### Example 1: Tandem synthesis of siNA constructs

Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in  
 25 high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the  
 30 oligonucleotides are deprotected as described above. Following deprotection, the siNA



sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even  
5 though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of  
10 introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is  
15 coupled, standard synthesis chemistry is utilized to complete synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M  $\text{NH}_4\text{H}_2\text{CO}_3$ .

Purification of the siNA duplex can be readily accomplished using solid phase  
20 extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1 column volume (CV) of acetonitrile, 2 CV  $\text{H}_2\text{O}$ , and 2 CV 50mM NaOAc. The sample is loaded and then washed with 1 CV  $\text{H}_2\text{O}$  or 50mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The column is then washed, for example with 1 CV  $\text{H}_2\text{O}$  followed by on-column  
25 detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with  $\text{H}_2\text{O}$  followed by 1 CV 1M NaCl and additional  
30  $\text{H}_2\text{O}$ . The siNA duplex product is then eluted, for example using 1 CV 20% aqueous CAN.

**Figure 2** provides an example of MALDI-TOF mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an

individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA construct only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

#### Example 2: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

Example 3: Selection of siNA molecule target sites in a RNA

The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

1. The target sequence is parsed *in silico* into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.
2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.
3. In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.
4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.

5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.
6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.
7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.
8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper (sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see **Tables II and III**). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.
9. The siNA molecules are screened in an *in vitro*, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

In an alternate approach, a pool of siNA constructs specific to a HCV target sequence is used to screen for target sites in cells expressing HCV RNA, such as the human hepatoma (Huh7) cells (see for example Randall *et al.*, 2003, *PNAS USA*, 100, 235-240). The general strategy used in this approach is shown in **Figure 9**. A non-limiting example of such is a pool comprising sequences having sequences comprising

SEQ ID NOS: 1-1681. Cells expressing HCV (e.g., Huh7 cells) are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with HCV inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example **Figure 7** and **Figure 8**). The  
 5 siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation, decreased HCV mRNA levels or decreased HCV protein expression), are sequenced to determine the most suitable target site(s) within the target HCV RNA sequence.

#### Example 4: HCV targeted siNA design

10 siNA target sites were chosen by analyzing sequences of the HCV RNA target and optionally prioritizing the target sites on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 3, or alternately by using an *in vitro* siNA system as described in Example 6 herein. siNA molecules were designed that could bind  
 15 each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA  
 20 duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration *in vivo* and/or improved pharmacokinetic, localization, and  
 25 delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity  
 30 using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-



evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 11**).

## 5 Example 5: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.*, US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 10 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.*, US Patent Nos. 6,111,086; 6,008,400; 15 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoroamidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O-Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.*, US Patent 5,631,360, incorporated by reference herein in its entirety). 20 25

During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'-direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside 30

phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is  
 5 then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5'-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency,  
 10 for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Usman et al., US 5,831,071, US 6,353,098, US 6,437,117, Bellon et al., US  
 15 6,054,576, US 6,162,909, US 6,303,773, and Scaringe *supra*, all of which are incorporated by reference herein in their entireties. Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade under inappropriate deprotection conditions. Such  
 20 oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

#### 25 Example 6: RNAi *in vitro* assay to assess siNA activity

An *in vitro* assay that recapitulates RNAi in a cell-free system is used to evaluate siNA constructs targeting HCV RNA targets. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with HCV target RNA. A *Drosophila* extract derived  
 30 from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*. Target RNA is generated via *in vitro* transcription from an appropriate HCV expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense

siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 min. at 90°C followed by 1 hour at 37°C, then diluted in lysis buffer (for example 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate).

5 Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM

10 final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug.ml creatine phosphokinase, 100 um GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-

15 assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25 x Passive Lysis Buffer (Promega). Target RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

20 Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [ $\alpha$ -<sup>32</sup>P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'-<sup>32</sup>P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage

25 products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager<sup>®</sup> quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

In one embodiment, this assay is used to determine target sites the HCV RNA

30 target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the HCV RNA target, for example, by

analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

#### Example 7: Nucleic acid inhibition of HCV target RNA *in vivo*

siNA molecules targeted to the huma HCV RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity *in vivo*, for example, using the following procedure. The target sequences and the nucleotide location within the HCV RNA are given in **Table II and III**.

Two formats are used to test the efficacy of siNAs targeting HCV. First, the reagents are tested in cell culture using, for example, Huh7 cells (see, for example, Randall *et al.*, 2003, *PNAS USA*, 100, 235-240) to determine the extent of RNA and protein inhibition. siNA reagents (*e.g.*; see **Tables II and III**) are selected against the HCV target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example, Huh7 cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (*eg.*, ABI 7700 Taqman®). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule.

In addition, a cell-plating format can be used to determine RNA inhibition. A non-limiting example of a multiple target screen to assay siNA mediated inhibition of HCV RNA is shown in **Figure 18**. siNA constructs (Table III) were transfected at 25 nM into Huh7 cells and HCV RNA quantitated compared to untreated cells (“cells” column in the figure) and cells transfected with lipofectamine (“LFA2K” column in the figure). As shown in Figure 18, several siNA constructs show significant inhibition of HCV RNA expression in the Huh7 replicon system. This system is described in Rice *et al.*, US 5,874,565 and US 6,127,116, both incorporated by reference herein.

#### Delivery of siNA to Cells

Huh7b cells stably transfected with the HCV subgenomic replicon Clone A or Ava.5 are seeded, for example, at  $8.5 \times 10^3$  cells per well of a 96-well plate in DMEM(Gibco) the day before transfection. siNA (final concentration, for example 25nM) and cationic lipid Lipofectamine2000 (e.g., final concentration 0.5ul/well) are complexed in Optimem (Gibco) at 37°C for 20 minutes in polypropylene microtubes. Following vortexing, the complexed siNA is added to each well and incubated for 24-72 hours.

#### Taqman quantification of mRNA

Total RNA is prepared from cells following siNA delivery, for example, using Ambion Rnaqueous 4-PCR purification kit for large scale extractions, or Ambion Rnaqueous-96 purification kit for 96-well assays. For Taqman analysis, dual-labeled probes are synthesized with, for example, the reporter dyes FAM or VIC covalently linked at the 5'-end and the quencher dye TAMARA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence detector using 50uL reactions consisting of 10uL total RNA, 100nM forward primer, 100nM reverse primer, 100nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5mM MgCl<sub>2</sub>, 100uM each dATP, dCTP, dGTP and dTTP, 0.2U RNase Inhibitor (Promega), 0.025U AmpliTaq Gold (PE-Applied Biosystems) and 0.2U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 minutes at 48°C, 10 minutes at 95°C, followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C. Quantitation of target mRNA level is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 30, 10 ng/rxn) and normalizing to, for example, 36B4 mRNA in either parallel or same tube TaqMan reactions. For HCV Replicon mRNA quantitation, PCR primers and probe specific for the neomycin gene were used:

neo-forward primer, 5'-CCGGCTACCTGCCCCATTC-3'; (SEQ ID NO: 1682)

neo-reverse primer, 5'-CCAGATCATCCTGATCGACAAG-3'; (SEQ ID NO: 1683)

neo-probe, 5'-FAM-ACATCGCATCGAGCGAGCACGTAC-TAMARA3'; (SEQ ID NO: 1684)

For normalization, 36B4 PCR primers and probe were used:

36B4-forward primer, 5'-TCTATCATCAACGGGTACAAACGA-3'; (SEQ ID NO: 1685)



36B4 reverse primer, 5'-CTTTTCAGCAAGTGGGAAGGTG-3'; (SEQ ID NO: 1686)

36B4 probe, 5'VIC-CCTGGCCTTGTCTGTGGAGACGGATTA-TAMARA3'; (SEQ ID NO: 1687)

## 5 Western blotting

Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and  
 10 pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody  
 15 for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

### Example 8: Models useful to evaluate the down-regulation of HCV gene expression

#### *Cell Culture*

20 Although there have been reports of replication of HCV in cell culture (see below), these systems are difficult to reproduce and have proven unreliable. Therefore, as was the case for development of other anti-HCV therapeutics, such as interferon and ribavirin, after demonstration of safety in animal studies applicant can proceed directly into a clinical feasibility study.

25 Several recent reports have documented *in vitro* growth of HCV in human cell lines (Mizutani *et al.*, *Biochem Biophys Res Commun* 1996 227(3):822-826; Tagawa *et al.*, *Journal of Gastroenterology and Hepatology* 1995 10(5):523-527; Cribier *et al.*, *Journal of General Virology* 76(10):2485-2491; Seipp *et al.*, *Journal of General Virology* 1997 78(10):2467-2478; Iacovacci *et al.*, *Research Virology* 1997 148(2):147-  
 30 151; Iacovacci *et al.*, *Hepatology* 1997 26(5) 1328-1337; Ito *et al.*, *Journal of General Virology* 1996 77(5):1043-1054; Nakajima *et al.*, *Journal of Virology* 1996 70(5):3325-

3329; Mizutani *et al.*, *Journal of Virology* 1996 70(10):7219-7223; Valli *et al.*, *Res Virol* 1995 146(4): 285-288; Kato *et al.*, *Biochem Biophys Res Comm* 1995 206(3):863-869). Replication of HCV has been reported in both T and B cell lines, as well as cell lines derived from human hepatocytes. Detection of low level replication was documented using either RT-PCR based assays or the b-DNA assay. It is important to note that the most recent publications regarding HCV cell cultures document replication for up to 6-months. However, the level of HCV replication observed in these cell lines has not been robust enough for screening of antiviral compounds.

In addition to cell lines that can be infected with HCV, several groups have reported the successful transformation of cell lines with cDNA clones of full-length or partial HCV genomes (Harada *et al.*, *Journal of General Virology*, 1995, 76(5)1215-1221; Haramatsu *et al.*, *Journal of Viral Hepatitis* 1997 4S(1):61-67; Dash *et al.*, *American Journal of Pathology* 1997 151(2):363-373; Mizuno *et al.*, *Gastroenterology* 1995 109(6):1933-40; Yoo *et al.*, *Journal Of Virology* 1995 69(1):32-38).

The recent development of subgenomic HCV RNA replicons capable of successfully replicating in the human hepatoma cell line, Huh7, represents a significant advance toward a dependable cell culture model. These replicons contain the neomycin gene upstream of the HCV nonstructural genes allowing for the selection of replicative RNAs in Huh7 cells. Initially, RNA replication was detected at a low frequency (Lohmann *et al.* *Science* 1999 285: 110-113) but the identification of replicons with cell-adaptive mutations in the NS5A region has improved the efficiency of replication 10,000-fold (Blight *et al.* *Science* 2000 290:1972-1975). Steps in the HCV life cycle, such as translation, protein processing, and RNA replication are recapitulated in the subgenomic replicon systems, but early events (viral attachment and uncoating) and viral assembly is absent. Inclusion of the structural genes of HCV within the replicons results in the production of HCV core and envelope proteins, but virus assembly does not occur (Pietschmann *et al.* *Journal of Virology* 2002 76: 4008-4021). Such replicon systems have been used to study siRNA mediated inhibition of HCV RNA, see for example, Randall *et al.*, 2003, *PNAS USA*, 100, 235-240.

In several cell culture systems, cationic lipids have been shown to enhance the bioavailability of oligonucleotides to cells in culture (Bennet, *et al.*, 1992, *Mol. Pharmacology*, 41, 1023-1033). In one embodiment, siNA molecules of the invention

are complexed with cationic lipids for cell culture experiments. siNA and cationic lipid mixtures are prepared in serum-free DMEM immediately prior to addition to the cells. DMEM plus additives are warmed to room temperature (about 20-25°C) and cationic lipid is added to the final desired concentration and the solution is vortexed briefly. siNA molecules are added to the final desired concentration and the solution is again vortexed briefly and incubated for 10 minutes at room temperature. In dose response experiments, the RNA/lipid complex is serially diluted into DMEM following the 10 minute incubation.

### *Animal Models*

Evaluating the efficacy of anti-HCV agents in animal models is an important prerequisite to human clinical trials. The best characterized animal system for HCV infection is the chimpanzee. Moreover, the chronic hepatitis that results from HCV infection in chimpanzees and humans is very similar. Although clinically relevant, the chimpanzee model suffers from several practical impediments that make use of this model difficult. These include high cost, long incubation requirements and lack of sufficient quantities of animals. Due to these factors, a number of groups have attempted to develop rodent models of chronic hepatitis C infection. While direct infection has not been possible, several groups have reported on the stable transfection of either portions or entire HCV genomes into rodents (Yamamoto *et al.*, Hepatology 1995 22(3): 847-855; Galun *et al.*, Journal of Infectious Disease 1995 172(1):25-30; Koike *et al.*, Journal of general Virology 1995 76(12):3031-3038; Pasquinelli *et al.*, Hepatology 1997 25(3): 719-727; Hayashi *et al.*, Princess Takamatsu Symp 1995 25:1430149; Mariya *et al.*, Journal of General Virology 1997 78(7) 1527-1531; Takehara *et al.*, Hepatology 1995 21(3):746-751; Kawamura *et al.*, Hepatology 1997 25(4): 1014-1021). In addition, transplantation of HCV infected human liver into immunocompromised mice results in prolonged detection of HCV RNA in the animal's blood.

A method for expressing hepatitis C virus in an *in vivo* animal model has been developed (Vierling, International PCT Publication No. WO 99/16307). Viable, HCV infected human hepatocytes are transplanted into a liver parenchyma of a scid/scid mouse host. The scid/scid mouse host is then maintained in a viable state, whereby viable, morphologically intact human hepatocytes persist in the donor tissue and hepatitis

C virus is replicated in the persisting human hepatocytes. This model provides an effective means for the study of HCV inhibition by enzymatic nucleic acids *in vivo*.

#### Example 9: RNAi mediated inhibition of HCV RNA expression

siNA constructs (e.g., siNA constructs shown in **Table III**) are tested for efficacy  
 5 in reducing HCV RNA expression in, for example, Huh7 cells (see, for example, Randall  
*et al.*, 2003, *PNAS USA*, 100, 235-240). Cells are plated approximately 24 hours before  
 transfection in 96-well plates at 5,000-7,500 cells/well, 100  $\mu$ l/well, such that at the time  
 of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed  
 with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50  $\mu$ l/well  
 10 and incubated for 20 minutes at room temperature. The siNA transfection mixtures are  
 added to cells to give a final siNA concentration of 25 nM in a volume of 150  $\mu$ l. Each  
 siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are  
 incubated at 37° for 24 hours in the continued presence of the siNA transfection mixture.  
 At 24 hours, RNA is prepared from each well of treated cells. The supernatants with the  
 15 transfection mixtures are first removed and discarded, then the cells are lysed and RNA  
 prepared from each well. Target gene expression following treatment is evaluated by  
 RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit)  
 for normalization. The triplicate data is averaged and the standard deviations determined  
 for each treatment. Normalized data are graphed and the percent reduction of target  
 20 mRNA by active siNAs in comparison to their respective inverted control siNAs is  
 determined.

In a non-limiting example, a siNA construct comprising ribonucleotides and 3'-  
 terminal dithymidine caps is assayed along with a chemically modified siNA construct  
 comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in  
 25 which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted  
 deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate  
 internucleotide linkage. Additional stabilization chemistries as described in Table IV are  
 similarly assayed for activity. These siNA constructs are compared to appropriate  
 matched chemistry inverted controls. In addition, the siNA constructs are also compared  
 30 to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells  
 transfected with lipid alone (transfection control).

Example 10: siNA Inhibition of a chimeric HCV/Poliovirus in HeLa Cells

Inhibition of a chimeric HCV/Poliovirus was investigated using 21 nucleotide siNA duplexes in HeLa cells. Seven siNA were designed that target three regions in the highly conserved 5' untranslated region (UTR) of HCV RNA. The siNAs were screened  
 5 in two cell culture systems dependent upon the 5'-UTR of HCV; one requires translation of an HCV/luciferase gene, while the other involves replication of a chimeric HCV/poliovirus (PV) (see Blatt *et al.*, USSN 09/740,332, filed December 18, 2000, incorporated by reference herein). Transfection for the HCV/PV system was performed in HeLa cells (grown in DMEM supplemented with sodium pyruvate and 100mM  
 10 HEPES with 5% FBS) using either cationic lipid NC168 or LFA2K, with an siNA concentration of 10nM or 25nM. HeLa cells were inoculated with HCV/PV virus at an moi=.01 pfu/cell for 30 minutes in serum-free media. The inoculum was removed and 80μL media was added, with 20μL of transfection complex added to each well. The cells and supernatants were frozen at 20-24 hours post transfection. Each plate  
 15 underwent 3 freeze-thaw cycles and the supernatant was collected. The supernatant was titered on HeLa cells for 3 days, then stained and counted. The results shown in Figures 14-17 are reported as pfu/ml x 10<sup>5</sup>.

Two siNAs (29579/29586 and 29578/2958) targeting the same region (shifted by one nucleotide) are active in both systems (see **Figure 12**). For example, a >85%  
 20 reduction in HCVPV replication was observed in siNA-treated cells compared to an inverse siNA control 29593/29600 (**Figure 12**) with an IC<sub>50</sub> = ~2.5 nM (**Figure 13**). To develop nuclease-resistant siNA for in vivo applications, siNAs can be modified to contain stabilizing chemical modifications. Such modifications include phosphorothioate linkages (P=S), 2'-O-methyl nucleotides, 2'-fluoro (F) nucleotides, 2'-deoxy  
 25 nucleotides, universal base nucleotides, 5' and/or 3' end modifications and a variety of other nucleotide and non-nucleotide modifications, such as those described herein, in one or both siNA strands. Using this systematic approach, active siNA molecules have been identified that are substantially more resistant to nucleases. Several of these constructs were tested in the HCV/poliovirus chimera system, demonstrating significant reduction  
 30 in viral replication (see **Figures 14-17**). siNA constructs shown in **Figures 14-17** are referred to by RPI#s that are cross referenced to **Table III**. siNA activity is compared to relevant controls (untreated cells, scrambled/inactive control sequences, or transfection



controls). **Figure 14** shows the inhibition of HCV RNA in the HCV/poliovirus chimera system using chemically modified siNA construct 30051/30053, which construct has inverted deoxy abasic nucleotides at the 3' and 5' ends, several phosphorothioate linkages, and 5-nitroindole nucleotides. **Figure 15** shows the inhibition of HCV RNA in the HCV/poliovirus chimera system using chemically modified siNA construct 30055/30057, which construct has inverted deoxy abasic nucleotides at the 3' and 5' ends, several phosphorothioate linkages, and 5-nitroindole nucleotides. **Figures 16 and 17** show the inhibition of HCV RNA in the HCV/poliovirus chimera system using unmodified siNA construct (29586/29579) and chemically modified siNA constructs 30417/30419, 30417/30420, 30418/30419, and combinations thereof at 10 nM and 25 nM siNA, respectively. As shown in **Figures 14-17**, siNA constructs of the invention provide potent inhibition of HCV RNA in the HCV/poliovirus chimera system. As such, siNA constructs, including chemically modified, nuclease resistant siNA molecules, represent an important class of therapeutic agents for treating chronic HCV infection.

#### 15 Example 11: siNA Inhibition of a HCV RNA expression in a HCV replicon system

A HCV replicon system was used to test the efficacy of siNAs targeting HCV RNA. The reagents are tested in cell culture using Huh7 cells (see for example Randall *et al.*, 2003, *PNAS USA*, 100, 235-240) to determine the extent of RNA and protein inhibition. siNA were selected against the HCV target as described herein. RNA inhibition was measured after delivery of these reagents by a suitable transfection agent to Huh7 cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (*eg.*, ABI 7700 Taqman®). A comparison is made to a mixture of oligonucleotide sequences designed to target unrelated targets or to a randomized siNA control with the same overall length and chemistry, but with randomly substituted nucleotides at each position. Primary and secondary lead reagents were chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition. A non-limiting example of a multiple target screen to assay siNA mediated inhibition of HCV RNA is shown in **Figure 18**. siNA reagents (Table I) were transfected at 25 nM into Huh7 cells and HCV RNA quantitated compared to untreated cells ("cells" column in the figure) and cells transfected with lipofectamine ("LFA2K"

column in the figure). As shown in the Figure, several siNA constructs show significant inhibition of HCV RNA expression in the Huh7 replicon system. Chemically modified siNA constructs were then screened as described above, with a non-limiting example of a Stab 7/8 (see **Table IV**) chemistry siNA construct screen shown in **Figure 20**. A follow up dose response study using chemically modified siNA constructs (Stab 4/5, see **Table IV**) at concentrations of 5nM, 10nM, 25 nM and 100 nM compared to matched chemistry inverted controls is shown in **Figure 19**, whereas a dose response study for Stab 7/8 constructs at concentrations of 5nM, 10nM, 25 nM, 50 nM and 100 nM compared to matched chemistry inverted controls is shown in **Figure 21**.

#### 10 Example 12: Effect of Interferon/siNA Combination Treatment on Replication of HCV Subgenomic Replicon in Huh7 Cells

To investigate combination use of RNAi and interferon in the inhibition of HCV replication, siNA and interferon combination treatments were assayed in the HCV Subgenomic Replicon in Huh7 cells. Huh7 cells containing the HCV subgenomic replicon Clone A were plated in 96-well plates at a density of 9,600 cells per well and incubated overnight at 37°C. The cells were then treated with interferon alone, siNAs or inverted sequence controls alone, or with interferon in combination with siNAs or inverted controls. A sub-optimal dose of interferon was used in order to observe possible potentiation of the interferon anti-viral activity in the presence of the HCV-targeted siNA. The cells were transfected with HCV targeted siNAs (31703/31707) or inverted sequence controls (31711/31715) at 5, 10, 25, 50, or 100 nM using 0.35 ul/well of Lipofectamine 2000 in media alone, or media to which was added 1.7 Units/ml of Infergen (Amgen). The cells were then incubated at 37°C for 48 or 72 hours, at which time total RNA was isolated using an Invitex 96-well RNA isolation kit. To quantitate the levels of RNA from the HCV replicon, real-time RT-PCR was performed using probes and primers to the neomycin resistance region of the replicon. Results are shown in **Figure 22**. Levels of the replicon RNA were normalized to the levels of cellular GAPDH mRNA. These data demonstrate potentiation of the effect of combination siNA/interferon treatment compared to interferon alone.

#### 30 Example 13: Indications

The present body of knowledge in HCV research indicates the need for methods to assay HCV activity and for compounds that can regulate HCV expression for research, diagnostic, and therapeutic use. As described herein, the nucleic acid molecules of the present invention can be used in assays to diagnose disease state related of HCV levels.

5 In addition, the nucleic acid molecules can be used to treat disease state related to HCV levels.

Particular degenerative and disease states that can be associated with HCV expression modulation include, but are not limited to, HCV infection, liver failure, hepatocellular carcinoma, cirrhosis, and/or other disease states associated with HCV  
10 infection.

#### Example 14: Interferons

Interferons represent a non-limiting example of a class of compounds that can be used in conjunction with the siNA molecules of the invention for treating the diseases and/or conditions described herein. Type I interferons (IFN) are a class of natural  
15 cytokines that includes a family of greater than 25 IFN- $\alpha$  (Pesta, 1986, *Methods Enzymol.* 119, 3-14) as well as IFN- $\beta$ , and IFN- $\omega$ . Although evolutionarily derived from the same gene (Diaz *et al.*, 1994, *Genomics* 22, 540-552), there are many differences in the primary sequence of these molecules, implying an evolutionary divergence in biologic activity. All type I IFN share a common pattern of biologic effects that begin  
20 with binding of the IFN to the cell surface receptor (Pfeffer & Strulovici, 1992, Transmembrane secondary messengers for IFN- $\alpha/\beta$ . In: *Interferon. Principles and Medical Applications.*, S. Baron, D.H. Coopenhaver, F. Dianzani, W.R. Fleischmann Jr., T.K. Hughes Jr., G.R. Kimpel, D.W. Niesel, G.J. Stanton, and S.K. Tying, eds. 151-160). Binding is followed by activation of tyrosine kinases, including the Janus tyrosine  
25 kinases and the STAT proteins, which leads to the production of several IFN-stimulated gene products (Johnson *et al.*, 1994, *Sci. Am.* 270, 68-75). The IFN-stimulated gene products are responsible for the pleotropic biologic effects of type I IFN, including antiviral, antiproliferative, and immunomodulatory effects, cytokine induction, and HLA class I and class II regulation (Pestka *et al.*, 1987, *Annu. Rev. Biochem* 56, 727).  
30 Examples of IFN-stimulated gene products include 2-5-oligoadenylate synthetase (2-5 OAS),  $\beta_2$ -microglobulin, neopterin, p68 kinases, and the Mx protein (Chebath & Revel,

1992, The 2-5 A system: 2-5 A synthetase, isospecies and functions. In: *Interferon. Principles and Medical Applications*, S. Baron, D.H. Coopenhaver, F. Dianzani, W.R. Jr. Fleischmann, T.K. Jr Hughes, G.R. Kimpel, D.W. Niesel, G.J. Stanton, and S.K. Tying, eds., pp. 225-236; Samuel, 1992, The RNA-dependent P1/eIF-2 $\alpha$  protein kinase. In: *Interferon. Principles and Medical Applications*. S. Baron, D.H. Coopenhaver, F. Dianzani, W.R. Fleischmann Jr., T.K. Hughes Jr., G.R. Kimpel, D.W. Niesel, G.H. Stanton, and S.K. Tying, eds. 237-250; Horisberger, 1992, MX protein: function and Mechanism of Action. In: *Interferon. Principles and Medical Applications*. S. Baron, D.H. Coopenhaver, F. Dianzani, W.R. Fleischmann Jr., T.K. Hughes Jr., G.R. Kimpel, D.W. Niesel, G.H. Stanton, and S.K. Tying, eds. 215-224). Although all type I IFN have similar biologic effects, not all the activities are shared by each type I IFN, and in many cases, the extent of activity varies quite substantially for each IFN subtype (Fish *et al.*, 1989, *J. Interferon Res.* 9, 97-114; Ozes *et al.*, 1992, *J. Interferon Res.* 12, 55-59). More specifically, investigations into the properties of different subtypes of IFN- $\alpha$  and molecular hybrids of IFN- $\alpha$  have shown differences in pharmacologic properties (Rubinstein, 1987, *J. Interferon Res.* 7, 545-551). These pharmacologic differences can arise from as few as three amino acid residue changes (Lee *et al.*, 1982, *Cancer Res.* 42, 1312-1316).

Eighty-five to 166 amino acids are conserved in the known IFN- $\alpha$  subtypes. Excluding the IFN- $\alpha$  pseudogenes, there are approximately 25 known distinct IFN- $\alpha$  subtypes. Pairwise comparisons of these nonallelic subtypes show primary sequence differences ranging from 2% to 23%. In addition to the naturally occurring IFNs, a non-natural recombinant type I interferon known as consensus interferon (CIFN) has been synthesized as a therapeutic compound (Tong *et al.*, 1997, *Hepatology* 26, 747-754).

Interferon is currently in use for at least 12 different indications, including infectious and autoimmune diseases and cancer (Borden, 1992, *N. Engl. J. Med.* 326, 1491-1492). For autoimmune diseases, IFN has been utilized for treatment of rheumatoid arthritis, multiple sclerosis, and Crohn's disease. For treatment of cancer, IFN has been used alone or in combination with a number of different compounds. Specific types of cancers for which IFN has been used include squamous cell carcinomas, melanomas, hypernephromas, hemangiomas, hairy cell leukemia, and Kaposi's sarcoma. In the treatment of infectious diseases, IFNs increase the phagocytic

activity of macrophages and cytotoxicity of lymphocytes and inhibits the propagation of cellular pathogens. Specific indications for which IFN has been used as treatment include hepatitis B, human papillomavirus types 6 and 11 (i.e. genital warts) (Leventhal *et al.*, 1991, *N Engl J Med* 325, 613-617), chronic granulomatous disease, and hepatitis C virus.

Numerous well controlled clinical trials using IFN-alpha in the treatment of chronic HCV infection have demonstrated that treatment three times a week results in lowering of serum ALT values in approximately 50% (range 40% to 70%) of patients by the end of 6 months of therapy (Davis *et al.*, 1989, *N. Engl. J. Med.* 321, 1501-1506; Marcellin *et al.*, 1991, *Hepatology* 13, 393-397; Tong *et al.*, 1997, *Hepatology* 26, 747-754; Tong *et al.*, *Hepatology* 26, 1640-1645). However, following cessation of interferon treatment, approximately 50% of the responding patients relapsed, resulting in a "durable" response rate as assessed by normalization of serum ALT concentrations of approximately 20 to 25%. In addition, studies that have examined six months of type 1 interferon therapy using changes in HCV RNA values as a clinical endpoint have demonstrated that up to 35% of patients will have a loss of HCV RNA by the end of therapy (Tong *et al.*, 1997, *supra*). However, as with the ALT endpoint, about 50% of the patients relapse six months following cessation of therapy resulting in a durable virologic response of only 12% (23). Studies that have examined 48 weeks of therapy have demonstrated that the sustained virological response is up to 25%.

Pegylated interferons, i.e., interferons conjugated with polyethylene glycol (PEG), have demonstrated improved characteristics over interferon. Advantages incurred by PEG conjugation can include an improved pharmacokinetic profile compared to interferons lacking PEG, thus imparting more convenient dosing regimes, improved tolerance, and improved antiviral efficacy. Such improvements have been demonstrated in clinical studies of both polyethylene glycol interferon alfa-2a (PEGASYS, Roche) and polyethylene glycol interferon alfa-2b (VIRAFERON PEG, PEG-INTRON, Enzon/Schering Plough).

siNA molecules in combination with interferons and polyethylene glycol interferons have the potential to improve the effectiveness of treatment of HCV or any of the other indications discussed above. siNA molecules targeting RNAs associated with



HCV infection can be used individually or in combination with other therapies such as interferons and polyethylene glycol interferons and to achieve enhanced efficacy.

Example 15: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes, siNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms

of target RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches

one skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

**Table I: HCV Accession Numbers**

Seq Nam	Acc#	LOCUS
gi 329763 gb M84754.1 HPCGENANTI	M84754.1	HPCGENANTI
gi 567059 gb U16362.1 HCU16362	U16362.1	HCU16362
gi 5918956 gb AF165059.1 AF165059	AF165059.1	AF165059
gi 385583 gb S62220.1 S62220	S62220.1	S62220
gi 6010587 gb AF177040.1 AF177040	AF177040.1	AF177040
gi 5748510 emb AJ238800.1 HCJ238800	AJ238800.1	HCJ238800
gi 7650221 gb AF207752.1 AF207752	AF207752.1	AF207752
gi 11559454 dbj AB049094.1 AB049094	AB049094.1	AB049094
gi 3550760 dbj D84263.1 D84263	D84263.1	D84263
gi 221610 dbj D90208.1 HPCJCG	D90208.1	HPCJCG
gi 558520 dbj D28917.1 HPCK3A	D28917.1	HPCK3A
gi 2176577 dbj E08461.1 E08461	E08461.1	E08461
gi 6707285 gb AF169005.1 AF169005	AF169005.1	AF169005
gi 12309923 emb AX057094.1 AX057094	AX057094.1	AX057094
gi 6010585 gb AF177039.1 AF177039	AF177039.1	AF177039
gi 7329202 gb AF238482.1 AF238482	AF238482.1	AF238482
gi 11559464 dbj AB049099.1 AB049099	AB049099.1	AB049099
gi 5918932 gb AF165047.1 AF165047	AF165047.1	AF165047
gi 5918946 gb AF165054.1 AF165054	AF165054.1	AF165054
gi 7650233 gb AF207758.1 AF207758	AF207758.1	AF207758
gi 19568932 gb AF483269.1	AF483269.1	
gi 7650247 gb AF207765.1 AF207765	AF207765.1	AF207765
gi 12309919 emb AX057086.1 AX057086	AX057086.1	AX057086
gi 5708597 dbj E10839.1 E10839	E10839.1	E10839
gi 2327074 gb AF011753.1 AF011753	AF011753.1	AF011753
gi 12310062 emb AX057317.1 AX057317	AX057317.1	AX057317
gi 221606 dbj D10750.1 HPCJ491	D10750.1	HPCJ491
gi 2174448 dbj E06261.1 E06261	E06261.1	E06261
gi 3098640 gb AF054251.1 AF054251	AF054251.1	AF054251
gi 18027684 gb AF313916.1 AF313916	AF313916.1	AF313916
gi 329873 gb M62321.1 HPCPLYPRE	M62321.1	HPCPLYPRE
gi 464177 dbj D14853.1 HPCCGS	D14853.1	HPCCGS
gi 15422182 gb AY051292.1	AY051292.1	
gi 676877 dbj D49374.1 HPCFG	D49374.1	HPCFG
gi 1030706 dbj D50480.1 HPCK1R1	D50480.1	HPCK1R1
gi 7650223 gb AF207753.1 AF207753	AF207753.1	AF207753
gi 7650237 gb AF207760.1 AF207760	AF207760.1	AF207760
gi 11559444 dbj AB049089.1 AB049089	AB049089.1	AB049089
gi 3550762 dbj D84264.1 D84264	D84264.1	D84264
gi 12831192 gb AF333324.1 AF333324	AF333324.1	AF333324
gi 13122265 dbj AB047641.1 AB047641	AB047641.1	AB047641
gi 7329204 gb AF238483.1 AF238483	AF238483.1	AF238483
gi 11559468 dbj AB049101.1 AB049101	AB049101.1	AB049101
gi 5918934 gb AF165048.1 AF165048	AF165048.1	AF165048
gi 5918948 gb AF165055.1 AF165055	AF165055.1	AF165055
gi 7650235 gb AF207759.1 AF207759	AF207759.1	AF207759
gi 7650249 gb AF207766.1 AF207766	AF207766.1	AF207766
gi 9843676 emb AJ278830.1 HEC278830	AJ278830.1	HEC278830
gi 11559450 dbj AB049092.1 AB049092	AB049092.1	AB049092
gi 2943783 dbj D89815.1 D89815	D89815.1	D89815

gi 9626438 ref NC_001433.1	NC_001433.1	
gi 12310134 emb AX057395.1 AX057395	AX057395.1	AX057395
gi 11559460 dbj AB049097.1 AB049097	AB049097.1	AB049097
gi 12309922 emb AX057092.1 AX057092	AX057092.1	AX057092
gi 2174644 dbj E06457.1 E06457	E06457.1	E06457
gi 2176559 dbj E08443.1 E08443	E08443.1	E08443
gi 5918960 gb AF165061.1 AF165061	AF165061.1	AF165061
gi 2326454 emb Y12083.1 HCV12083	Y12083.1	HCV12083
gi 5918938 gb AF165050.1 AF165050	AF165050.1	AF165050
gi 7650225 gb AF207754.1 AF207754	AF207754.1	AF207754
gi 7650261 gb AF207772.1 AF207772	AF207772.1	AF207772
gi 1030704 dbj D50485.1 HPCK1S2	D50485.1	HPCK1S2
gi 3550758 dbj D84262.1 D84262	D84262.1	D84262
gi 7650239 gb AF207761.1 AF207761	AF207761.1	AF207761
gi 3550764 dbj D84265.1 D84265	D84265.1	D84265
gi 7329206 gb AF238484.1 AF238484	AF238484.1	AF238484
gi 2176516 dbj E08399.1 E08399	E08399.1	E08399
gi 5918936 gb AF165049.1 AF165049	AF165049.1	AF165049
gi 11559446 dbj AB049090.1 AB049090	AB049090.1	AB049090
gi 5441837 emb AJ242653.1 SSE242653	AJ242653.1	SSE242653
gi 3098641 gb AF054252.1 AF054252	AF054252.1	AF054252
gi 4753720 emb AJ132997.1 HCV132997	AJ132997.1	HCV132997
gi 5420376 emb AJ238799.1 HCJ238799	AJ238799.1	HCJ238799
gi 11559440 dbj AB049087.1 AB049087	AB049087.1	AB049087
gi 15529110 gb AY045702.1	AY045702.1	
gi 560788 dbj D30613.1 HPCPP	D30613.1	HPCPP
gi 11225869 emb AX036253.1 AX036253	AX036253.1	AX036253
gi 11559456 dbj AB049095.1 AB049095	AB049095.1	AB049095
gi 329770 gb M58335.1 HPCHUMR	M58335.1	HPCHUMR
gi 6707279 gb AF169002.1 AF169002	AF169002.1	AF169002
gi 221586 dbj D10749.1 HPCHCJ1	D10749.1	HPCHCJ1
gi 2171981 dbj E03766.1 E03766	E03766.1	E03766
gi 6010579 gb AF177036.1 AF177036	AF177036.1	AF177036
gi 1030703 dbj D50484.1 HPCK1S3	D50484.1	HPCK1S3
gi 3098650 gb AF054257.1 AF054257	AF054257.1	AF054257
gi 5821154 dbj AB016785.1 AB016785	AB016785.1	AB016785
gi 5918962 gb AF165062.1 AF165062	AF165062.1	AF165062
gi 7650227 gb AF207755.1 AF207755	AF207755.1	AF207755
gi 7650263 gb AF207773.1 AF207773	AF207773.1	AF207773
gi 1183030 dbj D63822.1 HPCJK046E2	D63822.1	HPCJK046E2
gi 13122271 dbj AB047644.1 AB047644	AB047644.1	AB047644
gi 2443428 gb U89019.1 HCU89019	U89019.1	HCU89019
gi 2462303 emb Y13184.1 HCV1480	Y13184.1	HCV1480
gi 7329208 gb AF238485.1 AF238485	AF238485.1	AF238485
gi 1160327 dbj D14484.1 HPCJRNA	D14484.1	HPCJRNA
gi 12309921 emb AX057090.1 AX057090	AX057090.1	AX057090
gi 3098643 gb AF054253.1 AF054253	AF054253.1	AF054253
gi 21397075 gb AF511948.1	AF511948.1	
gi 1030701 dbj D50482.1 HPCK1R3	D50482.1	HPCK1R3
gi 1030702 dbj D50483.1 HPCK1S1	D50483.1	HPCK1S1
gi 3098632 gb AF054247.1 AF054247	AF054247.1	AF054247
gi 59478 emb X61596.1 HCVJK1G	X61596.1	HCVJK1G
gi 3098652 gb AF054258.1 AF054258	AF054258.1	AF054258
gi 5918950 gb AF165056.1 AF165056	AF165056.1	AF165056
gi 7650251 gb AF207767.1 AF207767	AF207767.1	AF207767



gi 5918964 gb AF165063.1 AF165063	AF165063.1	AF165063
gi 5918928 gb AF165045.1 AF165045	AF165045.1	AF165045
gi 5532421 gb AF139594.1 AF139594	AF139594.1	AF139594
gi 13122267 dbj AB047642.1 AB047642	AB047642.1	AB047642
gi 5441831 emb AJ242651.1 SSE242651	AJ242651.1	SSE242651
gi 7650265 gb AF207774.1 AF207774	AF207774.1	AF207774
gi 7650229 gb AF207756.1 AF207756	AF207756.1	AF207756
gi 1183032 dbj D63821.1 HPCJK049E1	D63821.1	HPCJK049E1
gi 2175714 dbj E07579.1 E07579	E07579.1	E07579
gi 1212741 dbj D45172.1 HPCHCPO	D45172.1	HPCHCPO
gi 5708511 dbj E05027.1 E05027	E05027.1	E05027
gi 1483141 dbj D50409.1 D50409	D50409.1	D50409
gi 13122261 dbj AB047639.1 AB047639	AB047639.1	AB047639
gi 6521008 dbj AB031663.1 AB031663	AB031663.1	AB031663
gi 633201 emb X76918.1 HCVCEMS1	X76918.1	HCVCEMS1
gi 329737 gb M67463.1 HPCCGAA	M67463.1	HPCCGAA
gi 11559452 dbj AB049093.1 AB049093	AB049093.1	AB049093
gi 13619567 emb AX100563.1 AX100563	AX100563.1	AX100563
gi 221604 dbj D13558.1 HPCJ483	D13558.1	HPCJ483
gi 11225872 emb AX036256.1 AX036256	AX036256.1	AX036256
gi 1749761 dbj D89872.1 D89872	D89872.1	D89872
gi 5918940 gb AF165051.1 AF165051	AF165051.1	AF165051
gi 4753718 emb AJ132996.1 HCV132996	AJ132996.1	HCV132996
gi 7650241 gb AF207762.1 AF207762	AF207762.1	AF207762
gi 3098645 gb AF054254.1 AF054254	AF054254.1	AF054254
gi 9930556 gb AF290978.1 AF290978	AF290978.1	AF290978
gi 11559462 dbj AB049098.1 AB049098	AB049098.1	AB049098
gi 2764397 emb AJ000009.1 HCVPOLYP	AJ000009.1	HCVPOLYP
gi 221608 dbj D10988.1 HPCJ8G	D10988.1	HPCJ8G
gi 3098634 gb AF054248.1 AF054248	AF054248.1	AF054248
gi 221650 dbj D00944.1 HPCPOLP	D00944.1	HPCPOLP
gi 306286 gb M96362.1 HPCUNKCDS	M96362.1	HPCUNKCDS
gi 3098654 gb AF054259.1 AF054259	AF054259.1	AF054259
gi 5918952 gb AF165057.1 AF165057	AF165057.1	AF165057
gi 7650253 gb AF207768.1 AF207768	AF207768.1	AF207768
gi 5918966 gb AF165064.1 AF165064	AF165064.1	AF165064
gi 15487693 gb AF356827.1 AF356827	AF356827.1	AF356827
gi 5738246 gb AF176573.1 AF176573	AF176573.1	AF176573
gi 11559448 dbj AB049091.1 AB049091	AB049091.1	AB049091
gi 21397077 gb AF511950.1	AF511950.1	
gi 3098638 gb AF054250.1 AF054250	AF054250.1	AF054250
gi 6707281 gb AF169003.1 AF169003	AF169003.1	AF169003
gi 329739 gb L02836.1 HPCCGENOM	L02836.1	HPCCGENOM
gi 6010581 gb AF177037.1 AF177037	AF177037.1	AF177037
gi 11559442 dbj AB049088.1 AB049088	AB049088.1	AB049088
gi 21397076 gb AF511949.1	AF511949.1	
gi 1030705 dbj D50481.1 HPCK1R2	D50481.1	HPCK1R2
gi 2176384 dbj E08264.1 E08264	E08264.1	E08264
gi 3660725 gb AF064490.1 AF064490	AF064490.1	AF064490
gi 2252489 emb Y11604.1 HCV4APOLY	Y11604.1	HCV4APOLY
gi 5918942 gb AF165052.1 AF165052	AF165052.1	AF165052
gi 2895898 gb AF046866.1 AF046866	AF046866.1	AF046866
gi 7650243 gb AF207763.1 AF207763	AF207763.1	AF207763
gi 11559458 dbj AB049096.1 AB049096	AB049096.1	AB049096
gi 13122263 dbj AB047640.1 AB047640	AB047640.1	AB047640

gi 5708574 dbj E08263.1 E08263	E08263.1	E08263
gi 7650257 gb AF207770.1 AF207770	AF207770.1	AF207770
gi 3098647 gb AF054255.1 AF054255	AF054255.1	AF054255
gi 11559466 dbj AB049100.1 AB049100	AB049100.1	AB049100
gi 1181831 gb U45476.1 HCU45476	U45476.1	HCU45476
gi 2327070 gb AF011751.1 AF011751	AF011751.1	AF011751
gi 3098636 gb AF054249.1 AF054249	AF054249.1	AF054249
gi 7329210 gb AF238486.1 AF238486	AF238486.1	AF238486
gi 221612 dbj D11168.1 HPCJTA	D11168.1	HPCJTA
gi 960359 dbj D63857.1 HPVHCVN	D63857.1	HPVHCVN
gi 13122273 dbj AB047645.1 AB047645	AB047645.1	AB047645
gi 5918954 gb AF165058.1 AF165058	AF165058.1	AF165058
gi 7650255 gb AF207769.1 AF207769	AF207769.1	AF207769
gi 437107 gb U01214.1 HCU01214	U01214.1	HCU01214
gi 471116 dbj D10934.1 HPCRNA	D10934.1	HPCRNA
gi 13026028 dbj E66593.1 E66593	E66593.1	E66593
gi 2316097 gb AF009606.1 AF009606	AF009606.1	AF009606
gi 6707283 gb AF169004.1 AF169004	AF169004.1	AF169004
gi 514395 dbj D17763.1 HPCEGS	D17763.1	HPCEGS
gi 9757541 dbj AB030907.1 AB030907	AB030907.1	AB030907
gi 7329200 gb AF238481.1 AF238481	AF238481.1	AF238481
gi 6010583 gb AF177038.1 AF177038	AF177038.1	AF177038
gi 2172621 dbj E04420.1 E04420	E04420.1	E04420
gi 8926244 gb AF271632.1 AF271632	AF271632.1	AF271632
gi 5918930 gb AF165046.1 AF165046	AF165046.1	AF165046
gi 7650231 gb AF207757.1 AF207757	AF207757.1	AF207757
gi 5918944 gb AF165053.1 AF165053	AF165053.1	AF165053
gi 7650245 gb AF207764.1 AF207764	AF207764.1	AF207764
gi 12309920 emb AX057088.1 AX057088	AX057088.1	AX057088
gi 5918958 gb AF165060.1 AF165060	AF165060.1	AF165060
gi 7650259 gb AF207771.1 AF207771	AF207771.1	AF207771
gi 7341102 gb AF208024.1 AF208024	AF208024.1	AF208024
gi 3098649 gb AF054256.1 AF054256	AF054256.1	AF054256
gi 1944375 dbj D85516.1 D85516	D85516.1	D85516
gi 2327072 gb AF011752.1 AF011752	AF011752.1	AF011752
gi 221614 dbj D11355.1 HPCJTB	D11355.1	HPCJTB
gi 13122269 dbj AB047643.1 AB047643	AB047643.1	AB047643

Table II: HCV siNA and Target Sequences

NM 000594 (hHCV)					
Sequence	SeqID	Upper seq	Seq ID	Lower seq	Seq ID
GCCCCGGAGGUCUCGUAG	1	GCCCCGGAGGUCUCGUAG	1	CUACGAGACCUCCGGGGC	697
UGUGGUACUGCCUGAUAGG	2	UGUGGUACUGCCUGAUAGG	2	CCUAUCAGGCAGUACCACA	698
UUGUGGUACUGCCUGAUAG	3	UUGUGGUACUGCCUGAUAG	3	CUAUCAGGCAGUACCACAA	699
CCCCGGGAGGUCUCGUAGA	4	CCCCGGGAGGUCUCGUAGA	4	UCUACGAGACCUCCGGGG	700
GUUGUACUGCCUGAUAGGG	5	GUUGUACUGCCUGAUAGGG	5	CCCUAUCAGGCAGUACCAC	701
CUGCCUGAUAGGGUGCUUG	6	CUGCCUGAUAGGGUGCUUG	6	CAAGCACCCUAUCAGGCAG	702
CCUUGUGGUACUGCCUGAU	7	CCUUGUGGUACUGCCUGAU	7	AUCAGGCAGUACCACAAGG	703
GCGAAAGGCCUUGUGGUAC	8	GCGAAAGGCCUUGUGGUAC	8	GUACCACAAGGCCUUUGC	704
UACUGCCUGAUAGGGUGCU	9	UACUGCCUGAUAGGGUGCU	9	AGCACCCUAUCAGGCAGUA	705
GGUACUGCCUGAUAGGGUG	10	GGUACUGCCUGAUAGGGUG	10	CACCCUAUCAGGCAGUACC	706
AAAGGCCUUGUGGUACUGC	11	AAAGGCCUUGUGGUACUGC	11	GCAGUACCACAAGGCCUUU	707
AAGGCCUUGUGGUACUGCC	12	AAGGCCUUGUGGUACUGCC	12	GGCAGUACCACAAGGCCUU	708
CUUGUGGUACUGCCUGAUA	13	CUUGUGGUACUGCCUGAUA	13	UAUCAGGCAGUACCACAAG	709
AGGCCUUGUGGUACUGCCU	14	AGGCCUUGUGGUACUGCCU	14	AGGCAGUACCACAAGGCCU	710
GUACUGCCUGAUAGGGUGC	15	GUACUGCCUGAUAGGGUGC	15	GCACCCUAUCAGGCAGUAC	711
ACUGCCUGAUAGGGUGCUU	16	ACUGCCUGAUAGGGUGCUU	16	AAGCACCCUAUCAGGCAGU	712
CUUGCGAGUGCCCCGGGAG	17	CUUGCGAGUGCCCCGGGAG	17	CUCCGGGGGCACUCGCAAG	713
CUGAUAGGGUGCUUUCGAG	18	CUGAUAGGGUGCUUUCGAG	18	CUCGCAAGCACCCUAUCAG	714
UUGCGAGUGCCCCGGGAGG	19	UUGCGAGUGCCCCGGGAGG	19	CCUCCGGGGGCACUCGCAA	715
CCUGAUAGGGUGCUUUCGA	20	CCUGAUAGGGUGCUUUCGA	20	UCGCAAGCACCCUAUCAGG	716
GGCCUUGUGGUACUGCCUG	21	GGCCUUGUGGUACUGCCUG	21	CAGGCAGUACCACAAGGCC	717
GCUUGCGAGUGCCCCGGGA	22	GCUUGCGAGUGCCCCGGGA	22	UCCCGGGGCACUCGCAAGC	718
UGCCUGAUAGGGUGCUUUC	23	UGCCUGAUAGGGUGCUUUC	23	GCAAGCACCCUAUCAGGCA	719
GAAAGGCCUUGUGGUACUG	24	GAAAGGCCUUGUGGUACUG	24	CAGUACCACAAGGCCUUUC	720
GCCUGAUAGGGUGCUUUCG	25	GCCUGAUAGGGUGCUUUCG	25	CGCAAGCACCCUAUCAGGC	721
CGAAAGGCCUUGUGGUACU	26	CGAAAGGCCUUGUGGUACU	26	AGUACCACAAGGCCUUUCG	722
GCCUUGUGGUACUGCCUGA	27	GCCUUGUGGUACUGCCUGA	27	UCAGGCAGUACCACAAGGC	723
GAGUGCCCCGGGAGGUCUC	28	GAGUGCCCCGGGAGGUCUC	28	GAGACCUCCCGGGGCACUC	724
CCCGGGAGGUCUCGUAGAC	29	CCCGGGAGGUCUCGUAGAC	29	GUCUACGAGACCUCCCGGG	725
UGCGAGUGCCCCGGGAGGU	30	UGCGAGUGCCCCGGGAGGU	30	ACCUCCCGGGGCACUCGCA	726

UGGUACUGCCUGAUAGGGU	31	UGGUACUGCCUGAUAGGGU	31	ACCCUAUCAGGCAGUACCA	727
CCGGUGAGUACACCGGAU	32	CCGGUGAGUACACCGGAU	32	AUCCGGUGUACUACCGG	728
GCGAGUGCCCCGGGAGGUC	33	GCGAGUGCCCCGGGAGGUC	33	GACCUCCCGGGGCACUCCG	729
CGAGUGCCCCGGGAGGUCU	34	CGAGUGCCCCGGGAGGUCU	34	AGACCUCCCGGGGCACUCG	730
UGCCCCGGGAGGUCUCGUA	35	UGCCCCGGGAGGUCUCGUA	35	UACGAGACCUCCCGGGGCA	731
GUCCCCCGGAGGUCUCGU	36	GUCCCCCGGAGGUCUCGU	36	ACGAGACCUCCCGGGGCAC	732
AGUGCCCCGGGAGGUCUCG	37	AGUGCCCCGGGAGGUCUCG	37	CGAGACCUCCCGGGGCACU	733
CCGGGAGGUCUCGUAGACC	38	CCGGGAGGUCUCGUAGACC	38	GGUCUACGAGACCUCCCGG	734
UGAUAGGGUGCUUGCGAGU	39	UGAUAGGGUGCUUGCGAGU	39	ACUCGCAAGCACCCUAUCA	735
GUUCUUGCGAGUGCCCCGG	40	GUUCUUGCGAGUGCCCCGG	40	CCGGGCACUCGCAAGCAC	736
AUAGGGUGCUUGCGAGUGC	41	AUAGGGUGCUUGCGAGUGC	41	GCACUCGCAAGCACCCUAU	737
GGGUGCUUGCGAGUGCCCC	42	GGGUGCUUGCGAGUGCCCC	42	GGGGCACUCGCAAGCACCC	738
CGGGAGGUCUCGUAGACCG	43	CGGGAGGUCUCGUAGACCG	43	CGGUCUACGAGACCUCCCG	739
GGGAGGUCUCGUAGACCGU	44	GGGAGGUCUCGUAGACCGU	44	ACGGUCUACGAGACCUCCC	740
GAUAGGGUGCUUGCGAGUG	45	GAUAGGGUGCUUGCGAGUG	45	CACUCGCAAGCACCCUAUC	741
GGAGGUCUCGUAGACCGUG	46	GGAGGUCUCGUAGACCGUG	46	CACGGUCUACGAGACCUCC	742
AGGGUGCUUGCGAGUGCCC	47	AGGGUGCUUGCGAGUGCCC	47	GGGCACUCGCAAGCACCCU	743
UGCUUGCGAGUGCCCCGGG	48	UGCUUGCGAGUGCCCCGGG	48	CCCGGGGCACUCGCAAGCA	744
GGUGCUUGCGAGUGCCCCG	49	GGUGCUUGCGAGUGCCCCG	49	CGGGGCACUCGCAAGCAC	745
UAGGGUGCUUGCGAGUGCC	50	UAGGGUGCUUGCGAGUGCC	50	GGCACUCGCAAGCACCCUA	746
AGGUCUCGUAGACCGUGCA	51	AGGUCUCGUAGACCGUGCA	51	UGCACGGUCUACGAGACCU	747
GAGGUCUCGUAGACCGUGC	52	GAGGUCUCGUAGACCGUGC	52	GCACGGUCUACGAGACCU	748
GGAACCGGUGAGUACACCG	53	GGAACCGGUGAGUACACCG	53	CGGUGUACUACACCGGUCC	749
CGGAACCGGUGAGUACACC	54	CGGAACCGGUGAGUACACC	54	GGUGUACUACACCGGUCCG	750
CGGUGAGUACACCGGAUU	55	CGGUGAGUACACCGGAUU	55	AUUCCGGUGUACUACACCG	751
GCGGAACCGGUGAGUACAC	56	GCGGAACCGGUGAGUACAC	56	GUUACUACACCGGUUCCGC	752
AACCGGUGAGUACACCGGA	57	AACCGGUGAGUACACCGGA	57	UCCGGUGUACUACACCGGU	753
ACCGGUGAGUACACCGGAA	58	ACCGGUGAGUACACCGGAA	58	UUCCGGUGUACUACACCGGU	754
CUGCGGAACCGGUGAGUAC	59	CUGCGGAACCGGUGAGUAC	59	GUACUACACCGGUUCCGCAG	755
GUUCUGCGGAACCGGUGAGU	60	GUUCUGCGGAACCGGUGAGU	60	ACUCACCGGUUCCGCAGAC	756
GAACCGGUGAGUACACCGG	61	GAACCGGUGAGUACACCGG	61	CCGGUGUACUACACCGGUUC	757
UGCGGAACCGGUGAGUACA	62	UGCGGAACCGGUGAGUACA	62	UGUACUACACCGGUUCCGCA	758
UCUGCGGAACCGGUGAGUA	63	UCUGCGGAACCGGUGAGUA	63	UACUACACCGGUUCCGCAGA	759
GGAGAGCCAUAGUGGUCU	64	GGAGAGCCAUAGUGGUCU	64	AGACCACUAUUGGUCUCC	760
GUUGGUCUGCGGAACCGGUG	65	GUUGGUCUGCGGAACCGGUG	65	CACCGGUUCCGCAGACCAC	761
GGUCUGCGGAACCGGUGAG	66	GGUCUGCGGAACCGGUGAG	66	CUCACCGGUUCCGCAGACC	762



CGGAGAGCCAUAGUGUC	67	CGGAGAGCCAUAGUGUC	67	GACCACU AUGGCUCCCG	763
CCGGAGAGCCAUAGUGU	68	CCGGAGAGCCAUAGUGU	68	ACCACU AUGGCUCCCG	764
UGGUCUGCGGAACCGGUA	69	UGGUCUGCGGAACCGGUA	69	UACCGGUUCCGACAGACA	765
GUGAGUACACCGGAUUGC	70	GUGAGUACACCGGAUUGC	70	GCAUUCGGUGUACUCAC	766
UGAGUACACCGGAUUGCC	71	UGAGUACACCGGAUUGCC	71	GGAUUCGGUGUACUCA	767
GGUGAGUACACCGGAUUG	72	GGUGAGUACACCGGAUUG	72	CAUUCGGUGUACUACC	768
GAGCCAUAGUGGUCUGCGG	73	GAGCCAUAGUGGUCUGCGG	73	CCGACAGACCACU AUGGCU	769
AGAGCCAUAGUGGUCUGCG	74	AGAGCCAUAGUGGUCUGCG	74	CGCAGACCACU AUGGCU	770
UAGUGGUCUGCGGAACCGG	75	UAGUGGUCUGCGGAACCGG	75	CCGGUCCGACAGACCACUA	771
AUAGUGGUCUGCGGAACCG	76	AUAGUGGUCUGCGGAACCG	76	CGGUUCCGACAGACCACUAU	772
GAGAGCCAUAGUGGUCUCG	77	GAGAGCCAUAGUGGUCUCG	77	GCAGACCACU AUGGCU	773
GCCAUAGUGGUCUGCGGAA	78	GCCAUAGUGGUCUGCGGAA	78	UUCGACAGACCACU AUGGC	774
AGUGGUCUGCGGAACCGGU	79	AGUGGUCUGCGGAACCGGU	79	ACCGGUUCCGACAGACCACU	775
CAUAGUGGUCUGCGGAACC	80	CAUAGUGGUCUGCGGAACC	80	GGUUCGACAGACCACU AUG	776
AGCCAUAGUGGUCUGCGGA	81	AGCCAUAGUGGUCUGCGGA	81	UCCGACAGACCACU AUGGCU	777
CCAUAGUGGUCUGCGGAAC	82	CCAUAGUGGUCUGCGGAAC	82	GUUCCGACAGACCACU AUGG	778
CCCCUCCCGGAGAGCCAU	83	CCCCUCCCGGAGAGCCAU	83	AUGGCUUCCCGGAGGGG	779
GGAGAGCCAUAGUGGUCUG	84	GGAGAGCCAUAGUGGUCUG	84	CAGACCACU AUGGCUCC	780
CCCGGAGAGCCAUAGUGG	85	CCCGGAGAGCCAUAGUGG	85	CCACU AUGGCUUCCCGGG	781
CCCCCUCCCGGAGAGCCA	86	CCCCCUCCCGGAGAGCCA	86	UGGCUUCCCGGAGGGGG	782
UCCCGGAGAGCCAUAGUG	87	UCCCGGAGAGCCAUAGUG	87	CACU AUGGCUUCCCGGGA	783
CCCCCUCCCGGAGAGGCC	88	CCCCCUCCCGGAGAGGCC	88	GGCUUCCCGGAGGGGG	784
CCCUCCCGGAGAGCCAU	89	CCCUCCCGGAGAGCCAU	89	UAUGGCUUCCCGGAGGG	785
CCUCCCGGAGAGCCAUAG	90	CCUCCCGGAGAGCCAUAG	90	CU AUGGCUUCCCGGAGG	786
CUCCCGGAGAGCCAUAGU	91	CUCCCGGAGAGCCAUAGU	91	ACU AUGGCUUCCCGGAG	787
UGUUGCCCGCAGGGGCC	92	UGUUGCCCGCAGGGGCC	92	GGGCCCUGCCGCGCAACA	788
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CAUGGCGUAGUAGUGUG	94	CAUGGCGUAGUAGUGUG	94	CACU CAUACU AACGCCAU	790
UAGCCAUUGGCGUAGUAG	95	UAGCCAUUGGCGUAGUAG	95	CAUACU AACGCCAU GGCUA	791
AGCCAUUGGCGUAGUAGA	96	AGCCAUUGGCGUAGUAGA	96	UCAUACU AACGCCAU GGCU	792
CCAUUGGCGUAGUAGAGU	97	CCAUUGGCGUAGUAGAGU	97	ACU CAUACU AACGCCAU GG	793
AUGGCGUAGUAGAGUGU	98	AUGGCGUAGUAGAGUGU	98	ACACU CAUACU AACGCCAU	794
AAGCGUCUAGCCAUUGCGU	99	AAGCGUCUAGCCAUUGCGU	99	ACGCCAUUGGCUAGACGCUU	795
GUUAGGCCAUUGCGUAGU	100	GUUAGGCCAUUGCGUAGU	100	ACU AACGCCAUUGGCUAGAC	796
AAAGCGUCUAGCCAUUGCG	101	AAAGCGUCUAGCCAUUGCG	101	CGCCAUUGGCUAGACGCUU	797
GCGUCUAGCCAUUGCGUUA	102	GCGUCUAGCCAUUGCGUUA	102	UAACGCCAUUGGCUAGACGC	798



GCCAUUGCGUUAAGUAG	103	GCCAUUGCGUUAAGUAG	103	CUCAUACUAACGCCAUGGC	799
AGCGUCUAGCCAUUGCGUU	104	AGCGUCUAGCCAUUGCGUU	104	AACGCCAUUGCUAGACGCU	800
CGUCUAGCCAUUGCGUUAAG	105	CGUCUAGCCAUUGCGUUAAG	105	CUAACGCCAUUGCUAGACG	801
UCUAGCCAUUGCGUUAAGUA	106	UCUAGCCAUUGCGUUAAGUA	106	UACUAAACGCCAUUGCUAGA	802
GAAAGCGUCUAGCCAUUGGC	107	GAAAGCGUCUAGCCAUUGGC	107	GCCAUUGCUAGACGCUUUC	803
CUAGCCAUUGCGUUAAGUAU	108	CUAGCCAUUGCGUUAAGUAU	108	AUACUAAACGCCAUUGGCUAG	804
CACUCCCCUGUAGGAACU	109	CACUCCCCUGUAGGAACU	109	AGUUCUCACAGGGGAGUG	805
ACCUCAAAAGAAAACCAA	110	ACCUCAAAAGAAAACCAA	110	UUUGUUUUUCUUUGAGGU	806
CGCAGAAAAGCGUCUAGCCA	111	CGCAGAAAAGCGUCUAGCCA	111	UGGCUAGACGCUUUCUGCG	807
GGGUAAGGUCAUCGAUACC	112	GGGUAAGGUCAUCGAUACC	112	GGUAUCGAUAGACCUUACCC	808
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GUAAAGGUCAUCGAUACCCU	120	GUAAAGGUCAUCGAUACCCU	120	AGGUUUCGAUGACCUUAC	816
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GGUAAGGUCAUCGAUACCC	122	GGUAAGGUCAUCGAUACCC	122	GGGUUUCGAUGACCUUACCC	818
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UCACUCCCCUGUGAGGAAC	124	UCACUCCCCUGUGAGGAAC	124	GUUCCUCACAGGGGAGUGA	820
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CACGCAGAAAAGCGUCUAGC	127	CACGCAGAAAAGCGUCUAGC	127	GCUAGACGCUUUCUGCGUG	823
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AGGAACUACUGUCUUCACG	134	AGGAACUACUGUCUUCACG	134	CGUGAAGACAGUAGUUCU	830
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GU AUGAGUGUGUGGAGACC	320	GU AUGAGUGUGUGGAGACC	320	GGCUGCAGCAGACUCAUAC	1016
AUGAGUGUGUGGAGCCUC	321	AUGAGUGUGUGGAGCCUC	321	GAGGCUAGCAGACACUCAU	1017
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GACCCCCCUCCCGGGAGA	327	GACCCCCCUCCCGGGAGA	327	UCUCCCGGGAGGGGGGUC	1023
CGGGUCCUUCUUGGAUCA	328	CGGGUCCUUCUUGGAUCA	328	UGAUCCAAAGAAAGACCCG	1024
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CAACCGCCGCCACAGAGAC	516	CAACCGCCGCCACAGAGAC	516	GUCCUGUGGGCGGCGGUUG	1212
UGCGGCUUCGCCGACCUC	517	UGCGGCUUCGCCGACCUC	517	UGAGGUCGGCGGAAGCCGCA	1213
CGGUGGUCAGAUCCGUUGGU	518	CGGUGGUCAGAUCCGUUGGU	518	ACCAACGAUCUGACCACCG	1214
UUGGGUGUGCGCGGACUA	519	UUGGGUGUGCGCGGACUA	519	UAGUCGCGGCACACCCAA	1215
GUGUGCGCGGACUAAGAA	520	GUGUGCGCGGACUAAGAA	520	UUCCUAGUCGCGGCACAC	1216
GAUGGCUCCUGUACCCCG	521	GAUGGCUCCUGUACCCCG	521	CGGGGUGACAGGAGCCAUC	1217
GGAUGGCUCCUGUACCCCG	522	GGAUGGCUCCUGUACCCCG	522	GGGGUGACAGGAGCCAUCC	1218
UGUGCGCGGACUAGGAAG	523	UGUGCGCGGACUAGGAAG	523	CUUCCUAGUCGCGGCACACA	1219
UGGGUGUGCGCGGACUAG	524	UGGGUGUGCGCGGACUAG	524	CUAGUCGCGGCACACCCA	1220
GGUGUGCGCGGACUAGGA	525	GGUGUGCGCGGACUAGGA	525	UCCUAGUCGCGGCACACAC	1221
GCGUGUGCGCGGACUAGG	526	GCGUGUGCGCGGACUAGG	526	CCUAGUCGCGGCACACCCC	1222
CCCCGGCGUAGGUGCGGUA	527	CCCCGGCGUAGGUGCGGUA	527	UACGGACCUACGCCGGGG	1223
GAAGGCGACAACCUAUCCC	528	GAAGGCGACAACCUAUCCC	528	GGAUAGGUAUUGUGCCCUUC	1224
CCCCGGCUAGGUGCGGUAA	529	CCCCGGCUAGGUGCGGUAA	529	UUACGGGACCUACGCCGGG	1225
AGCGGAGACGGCUGGAGCG	530	AGCGGAGACGGCUGGAGCG	530	CGCUCCAGCCGUCUCCGCU	1226
CCCCCGGCGUAGGUCGCGU	531	CCCCCGGCGUAGGUCGCGU	531	ACGCGACCUACGCCGGGGG	1227
AGGCGAAGGCGUCCACAGU	532	AGGCGAAGGCGUCCACAGU	532	ACUGUGGAGCGCCUUCGCCU	1228
AAGCGAAGGCGUCCACAG	533	AAGCGAAGGCGUCCACAG	533	CUGUGGACGCGCCUUCGCCU	1229
GUUGGGUGUGCGCGGACU	534	GUUGGGUGUGCGCGGACU	534	AGUCCGCGCGACACCCCAAC	1230

CUCAUUGGGGUACAUUCGCG	535	CUCAUUGGGGUACAUUCGCG	535	GCGGAUGUACCCCAUGAG	1231
GGAAGGCGACAACCUAUCC	536	GGAAGGCGACAACCUAUCC	536	GGAUAGGUUGUGGCCUUC	1232
GCAAGUUCUUGCCGACGG	537	GCAAGUUCUUGCCGACGG	537	CCGUCCGCCAAGGAACUUGC	1233
UGCAGCCUCCAGACCCCGC	538	UGCAGCCUCCAGACCCCGC	538	GGGGUCCUGGAGGCUGCA	1234
GGACUGCACGAUGCUCGUG	539	GGACUGCACGAUGCUCGUG	539	CACGAGCAUCGUGCAGUCC	1235
GAAAGCGAAGCGCUGCCACA	540	GAAAGCGAAGCGCUGCCACA	540	UGUGAGCGCCUUCGCCUUC	1236
GCAACCUUGUGGAAAGCGCA	541	GCAACCUUGUGGAAAGCGCA	541	UCGCCUUCACGAGGUUGC	1237
GACGCGGGCUUGCUUGGU	542	GACGCGGGCUUGCUUGGU	542	ACCAAGCACAGCCCGCGUC	1238
ACGCGGGCUUGCUUGGUA	543	ACGCGGGCUUGCUUGGUA	543	UACCAAGCACAGCCCGCGU	1239
GUGCAGCCUCCAGGACCCC	544	GUGCAGCCUCCAGGACCCC	544	GGGGUCCUGGAGGCUGCAC	1240
GCAGCCUCCAGGACCCCGC	545	GCAGCCUCCAGGACCCCGC	545	GGGGGUCCUGGAGGCUGC	1241
CGCAACCUUGUGGAAGGCG	546	CGCAACCUUGUGGAAGGCG	546	CGCCUCCACGAGGUUGCG	1242
UGUCGUGCAGCCUCCAGGA	547	UGUCGUGCAGCCUCCAGGA	547	UCCUGGAGGCUGCACGACA	1243
AUGGCUUGGGAUAUGAUGA	548	AUGGCUUGGGAUAUGAUGA	548	UCAUCAUAUCCCAAGCCAU	1244
CUUGGGAUAUGAUGAUGAA	549	CUUGGGAUAUGAUGAUGAA	549	UUCAUCAUAUCCCAAG	1245
CCCUUGGCCCCUCUAUGGC	550	CCCUUGGCCCCUCUAUGGC	550	GCCAUAAGAGGGGCCAAGGG	1246
UGGCUUGGGAUAUGAUGAU	551	UGGCUUGGGAUAUGAUGAU	551	AUCAUCAUAUCCCAAGCCA	1247
CUGUGCAGUGGAUGAACCG	552	CUGUGCAGUGGAUGAACCG	552	CGGUUCAUCCACUUGCACAG	1248
AUGACGCGGGCUUGGCUUG	553	AUGACGCGGGCUUGGCUUG	553	CAAGCACAGCCCGCGUCAU	1249
GCUUGGGAUAUGAUGAUGA	554	GCUUGGGAUAUGAUGAUGA	554	UCAUCAUCAUAUCCCAAGC	1250
UAUGACGCGGGCUUGGCUU	555	UAUGACGCGGGCUUGGCUU	555	AAGCACAGCCCGCGUCAUA	1251
UGACGCGGGCUUGGCUUGG	556	UGACGCGGGCUUGGCUUGG	556	CCAAGCACAGCCCGCGUCA	1252
GGCUUGGGAUAUGAUGAUG	557	GGCUUGGGAUAUGAUGAUG	557	CAUCAUCAUAUCCCAAGCC	1253
UGUGCAGUGGAUGAACCGG	558	UGUGCAGUGGAUGAACCGG	558	CCGGUUCAUCCACUUGCACA	1254
GCUUGCAGUGGAUGAACCC	559	GCUUGCAGUGGAUGAACCC	559	GGUUCAUCCACUGCACAGC	1255
CUCUUCAACUGGGCAGUAA	560	CUCUUCAACUGGGCAGUAA	560	UUACUGCCCAGUUGAAGAG	1256
CCUCGUGGAAGGCGACAAC	561	CCUCGUGGAAGGCGACAAC	561	GUUGUGGCCUUCACACGAGG	1257
UGUGUACCCAGACAGUGCG	562	UGUGUACCCAGACAGUGCG	562	CGACUGUCUGGGUGACACA	1258
GGCGUGAACUAUGCAACAG	563	GGCGUGAACUAUGCAACAG	563	CUGUGCAUAAGUUCACGCC	1259
CGGCGUGAACUAUGCAACA	564	CGGCGUGAACUAUGCAACA	564	UGUUGCAUAAGUUCACGCCG	1260
GUGUCACCCAGACAGUCGA	565	GUGUCACCCAGACAGUCGA	565	UCGACUGUCUGGGUGACAC	1261
CCUCUUCAACUGGGCAGUA	566	CCUCUUCAACUGGGCAGUA	566	UACUGCCCAAGUUGAAGAGG	1262
CGUGGAAGGCGACAACCUA	567	CGUGGAAGGCGACAACCUA	567	UAGGUUGUGGCCUUCACAG	1263
UCGUGGAAGGCGACAACCU	568	UCGUGGAAGGCGACAACCU	568	AGGUUGUGGCCUUCACAGA	1264
CGGCCUAGUUGGGCCCA	569	CGGCCUAGUUGGGCCCA	569	UGGGGCCCAACUAAGGCCG	1265
CGACUAGGAAGACUUCCGA	570	CGACUAGGAAGACUUCCGA	570	UCGGAAGUCUUCCUAGUCG	1266



UUUGGUUAGGUCAUCGAU	571	UUUGGUUAGGUCAUCGAU	571	AUCGAUGACCUUACCCAAA	1267
GUUGAAGGCGACAACCUAU	572	GUUGAAGGCGACAACCUAU	572	AUAGGUUGUGGCCUUCAC	1268
ACCUCGUGGAAGGCGACAA	573	ACCUCGUGGAAGGCGACAA	573	UUGUCGCCUUCACGAGGU	1269
GCGACUAGGAAGACUUCG	574	GCGACUAGGAAGACUUCG	574	CGGAAGUCCUAGUCCG	1270
GUUGUGCAGCCUCCAGGAC	575	GUUGUGCAGCCUCCAGGAC	575	GUCCUGGAGGCUGCACGAC	1271
UAGGAAGACUUCGAGCGG	576	UAGGAAGACUUCGAGCGG	576	CCGCUCGGAAGUCUCCUA	1272
ACGGCGUGAACUAUGCAAC	577	ACGGCGUGAACUAUGCAAC	577	GUUGCAUAGUUCACGCCGU	1273
CUUGUGAAGGCGACAACC	578	CUUGUGAAGGCGACAACC	578	GGUUGUGCCCUUCACGAG	1274
GGUCGCAACCUUGUGAAG	579	GGUCGCAACCUUGUGAAG	579	CUUCCACGAGGUUGCAC	1275
CGGUCGCAACCUCGUGGAA	580	CGGUCGCAACCUCGUGGAA	580	UUCACGAGGUUGCAGCCG	1276
GCGCGCGACUAGGAAGACU	581	GCGCGCGACUAGGAAGACU	581	AGUCUUCCUAGUGCGCGC	1277
GACGGCGUGAACUAUGCAA	582	GACGGCGUGAACUAUGCAA	582	UUGCAUAGUUCACGCCGUC	1278
UAGAUCAUCUCCCUUGUAG	583	UAGAUCAUCUCCCUUGUAG	583	CUACAGGGGAGUGAUCUA	1279
AGCGGUCCGAACCUUGUGG	584	AGCGGUCCGAACCUUGUGG	584	CCACGAGGUUGCAGCCGU	1280
UGGAAGGCGACAACCUAUC	585	UGGAAGGCGACAACCUAUC	585	GAUAGGUUGUCGCCUCCA	1281
CGGCGGACUAGGAAGACUU	586	CGGCGGACUAGGAAGACUU	586	AAGUUUCCUAGUCCGCGG	1282
CUAGGAAGACUUCCGAGCG	587	CUAGGAAGACUUCCGAGCG	587	CGCUCCGGAAGUCUCCUAG	1283
GUUGCGCGGACUAGGAAGA	588	GUUGCGCGGACUAGGAAGA	588	UCUUCCUAGUCCGCGGCAC	1284
AGAUCAUCUCCCUUGUAGG	589	AGAUCAUCUCCCUUGUAGG	589	CCUCACAGGGGAGUGAUCU	1285
UGCGCGCGACUAGGAAGAC	590	UGCGCGCGACUAGGAAGAC	590	GUUUCCUAGUCCGCGCA	1286
AUAGAUCAUCUCCCUUGUA	591	AUAGAUCAUCUCCCUUGUA	591	UCACAGGGGAGUGAUCUAU	1287
GAGCGGUCGCAACCUUGUG	592	GAGCGGUCGCAACCUUGUG	592	CACGAGGUUGCAGCCGUC	1288
CACGAACGACUGCUCCAAC	593	CACGAACGACUGCUCCAAC	593	GUUGAGGAGUCCGUUCGUG	1289
GGCAAGUUCCUUGCCGACG	594	GGCAAGUUCCUUGCCGACG	594	CGUCCGGCAAGGAACUUGCC	1290
UCGUGCAGCCUCCAGGACC	595	UCGUGCAGCCUCCAGGACC	595	GGUCCUGAGGCGUCACGA	1291
GUACAGGAACGACUGCUCCA	596	GUACAGGAACGACUGCUCCA	596	UGGAGCAGUCGUUCGUGAC	1292
GCGGUCGCAACCUUGUGGA	597	GCGGUCGCAACCUUGUGGA	597	UCCACGAGGUUGCACCGC	1293
GCGCGACUAGGAAGACUUC	598	GCGCGACUAGGAAGACUUC	598	GAAGUCUUCCUAGUCGCGC	1294
GCUAUGACGCGGCGUGUGC	599	GCUAUGACGCGGCGUGUGC	599	GCACAGCCCGCGUCAUAGC	1295
UCACGAACGACUGCUCAA	600	UCACGAACGACUGCUCAA	600	UUGAGCAGUUCGUUCGUA	1296
UCCGAACCUUGGGAAGGC	601	UCCGAACCUUGGGAAGGC	601	GCCUUCACGAGGCUUGCGA	1297
CGUGCAGCCUCCAGGACCC	602	CGUGCAGCCUCCAGGACCC	602	GGGUCCUGGAGGCGUCACG	1298
GUUGCAACCUUGGGAAGG	603	GUUGCAACCUUGGGAAGG	603	CCUUCACGAGGUUGCGAC	1299
ACUAGGAAGACUUCGAGC	604	ACUAGGAAGACUUCGAGC	604	GCUCGGAAGUCCUCCUAGU	1300
CGGACUAGGAAGACUUC	605	CGGACUAGGAAGACUUC	605	GGAAGUCCUCCUAGUCCG	1301
UGGCGGAAGCACAUUGUGA	606	UGGCGGAAGCACAUUGUGA	606	UCCACAUGUGCUUCGCCCA	1302

CCUUGCCUACUAUUCCAUG	607	CCUUGCCUACUAUUCCAUG	607	CAUGGAUAGUAGGCAAGG	1303
GCCUCAGGAAACUUGGGGU	608	GCCUCAGGAAACUUGGGGU	608	ACCCCAAGUUUCCUGAGGC	1304
UGCUAUGACGCGGGCUUG	609	UGCUAUGACGCGGGCUUG	609	CACAGCCCGCGUCAUAGCA	1305
UCGUGCUGCCACCUGCUC	610	UCGUGCUGCCACCUGCUC	610	GUAGCGGUGCGGAGCACGA	1306
UGCCUCAGGAAACUUGGGG	611	UGCCUCAGGAAACUUGGGG	611	CCCCAAGUUUCCUGAGGCA	1307
UGUCUCGUGCCCGACCCCG	612	UGUCUCGUGCCCGACCCCG	612	CGGGGUCGGGCACGAGACA	1308
UGUGGCGGCAAGAUUGGG	613	UGUGGCGGCAAGAUUGGG	613	CCCAUUCUCCUGCCGCCACA	1309
GUUGUGCUCCGCCACCGCUA	614	GUUGUGCUCCGCCACCGCUA	614	UAGCGGUGGCGAGCACGAC	1310
GAUUUCCACUACGUGACGG	615	GAUUUCCACUACGUGACGG	615	CCGUCACGUAGUGGAAAUUC	1311
GGCCCUUGCCUACUAUUCC	616	GGCCCUUGCCUACUAUUCC	616	GGAUAUAGUAGGCAAGGCC	1312
GCCUUGCCUACUAUUCCA	617	GCCUUGCCUACUAUUCCA	617	AUGGAUAUAGGCAAGGC	1313
GACUAGGAAGACUUCCGAG	618	GACUAGGAAGACUUCCGAG	618	CUCGGAAUUCUUCCUAGUC	1314
GCGGGGAGACAUUAUACA	619	GCGGGGAGACAUUAUACA	619	UGAUUAUAGUUCUCCCCCGC	1315
CGAGCGGUGCGAACCUUCGU	620	CGAGCGGUGCGAACCUUCGU	620	ACGAGGUUGCGACCGCUCG	1316
GGCCUUGCCUACUAUUCCA	621	GGCCUUGCCUACUAUUCCA	621	UGGAUAUAGUAGGCAAGGCC	1317
AUUUCCACUACGUGACGGG	622	AUUUCCACUACGUGACGGG	622	CCCGUACACGUAGUGGAAAU	1318
GGACGUCAAGUUCCCGGGC	623	GGACGUCAAGUUCCCGGGC	623	GCCCCGGGAACUUGACGUCC	1319
GAGUGCUAUGACGCGGGCU	624	GAGUGCUAUGACGCGGGCU	624	AGCCCCGUCAUUAGCACUC	1320
GACGUCAAAGUUCCCGGGCG	625	GACGUCAAAGUUCCCGGGCG	625	CGCCCCGGAACUUGACGUC	1321
UCAGCGACGGGUCUUGGUC	626	UCAGCGACGGGUCUUGGUC	626	GACCAAGACCCGUCGCUGA	1322
UCAAGUUCCCGGGCGGUGG	627	UCAAGUUCCCGGGCGGUGG	627	CCACCGCCCCGGGAACUUGA	1323
UCAAGGAGAUGAAGGCCGAA	628	UCAAGGAGAUGAAGGCCGAA	628	UUCGCCUUCAUCUCCUUGA	1324
CCUAUCCCCAAGGCUCCGCC	629	CCUAUCCCCAAGGCUCCGCC	629	GCGGAGCCUUGGGGAUAGG	1325
CUUGACCUACCUCAGAUCA	630	CUUGACCUACCUCAGAUCA	630	UGAUCUGAGGUAGGUCAAG	1326
UUUCCACUACGUGACGGGC	631	UUUCCACUACGUGACGGGC	631	GCCCCGUACGUAGUGGAAA	1327
AGUGCUAUGACGCGGGCUG	632	AGUGCUAUGACGCGGGCUG	632	CAGCCCGCGUCAUAGCACU	1328
ACGUCAAGUUCCCGGGCGG	633	ACGUCAAGUUCCCGGGCGG	633	CCGCCCGGGAACUUGACGU	1329
UCUGGAGACAUCCGGCCAG	634	UCUGGAGACAUCCGGCCAG	634	CUGGCCCCGAUUGUCUCCAGA	1330
GGCGGAAGCACAUUGUGGAA	635	GGCGGAAGCACAUUGUGGAA	635	UUCCACAUGUGCUUCCGCC	1331
UUGACCUCUACCUCAGAUCAU	636	UUGACCUCUACCUCAGAUCAU	636	AUGAUCUGAGGUAGGUCAA	1332
CCAAGCGGAGACGGCUGGA	637	CCAAGCGGAGACGGCUGGA	637	UCCAAGCGUCUCCGCUUGG	1333
ACCAAGCGGAGACGGCUGG	638	ACCAAGCGGAGACGGCUGG	638	CCAGCCGUCUCCGCUUGGU	1334
GGGUGGCUUCAUGCCUCAG	639	GGGUGGCUUCAUGCCUCAG	639	CUGAGGCAUGAAGCCACCC	1335
GUCAAGUUCCCGGGCGGUG	640	GUCAAGUUCCCGGGCGGUG	640	CACCGCCCCGGAACUUGAC	1336
CUCAAAGGAGAUGAAGGCCA	641	CUCAAAGGAGAUGAAGGCCA	641	UCGCCUUCAUCUCCUUGAG	1337
GACCAAGCGGAGACGGCUG	642	GACCAAGCGGAGACGGCUG	642	CAGCCGUCUCCGCUUGGUC	1338



UCCAGGUCGGGCUCAACCA	643	UCCAGGUCGGGCUCAACCA	643	UGGUGAGCCCGACCUGGA	1339
CUUUUUUCUAUUCUUCUC	644	CUUUUUUCUAUUCUUCUC	644	GAGGAAGUAAGAGAAAGAG	1340
GUCUGGAGACAUCGGGCCA	645	GUCUGGAGACAUCGGGCCA	645	UGGCCCGAUGUCUCCAGAC	1341
GUUGUGACUUGGCCCCGA	646	GUUGUGACUUGGCCCCGA	646	UCGGGGCCAAAGUCACAAC	1342
AGACCUGGCUCCAGUCCAA	647	AGACCUGGCUCCAGUCCAA	647	UUGGACUGGAGCCAGGUCU	1343
CUUGCCUACUAUUCCAUGG	648	CUUGCCUACUAUUCCAUGG	648	CCAUGGAUAAGUAGGCAAG	1344
CCCGGUUGCUUUUCUUA	649	CCCGGUUGCUUUUCUUA	649	UAGAGAAAGAGCAACCGGG	1345
CUUUCUCUAUCUUCUCUU	650	CUUUCUCUAUCUUCUCUU	650	AAGAGGAAGUAAGAGAAAG	1346
AGGGUGGCUUCAUGCCUCA	651	AGGGUGGCUUCAUGCCUCA	651	UGAGGCAUGAAAGCCACCCU	1347
AAGACCUGGCUCACAGUCCA	652	AAGACCUGGCUCACAGUCCA	652	UGGACUGGAGCCAGGUCUU	1348
CCGGUUGCUUUUCUUAU	653	CCGGUUGCUUUUCUUAU	653	AUAGAGAAAAGAGCAACCGG	1349
CGGUUGCUCUUUCUUAUC	654	CGGUUGCUCUUUCUUAUC	654	GAUAGAGAAAAGAGCAACCG	1350
UGGGGAUUUCCACUACGU	655	UGGGGAUUUCCACUACGU	655	ACGUAGUGGAAAUCCCCCA	1351
AUGUCACGAACGACUUGCUC	656	AUGUCACGAACGACUUGCUC	656	GAGCAGUCGUUCGUAGACAU	1352
GGCCUAGUUGGGGCCCCAC	657	GGCCUAGUUGGGGCCCCAC	657	GUGGGGCCCCCAACUAGGCC	1353
UGGACCAAAGCGGAGACGGC	658	UGGACCAAAGCGGAGACGGC	658	GCCGUCUCCGCUUGGUCCA	1354
UUCCAGGUCGGGCUCAACC	659	UUCCAGGUCGGGCUCAACC	659	GGUUGAGCCCCGACCUUGAA	1355
AGCGGUCGAGUUCUUGGU	660	AGCGGUCGAGUUCUUGGU	660	ACCAAGAACUCGACCCGCU	1356
CAAGGAGAUGAAGGCGGAAG	661	CAAGGAGAUGAAGGCGGAAG	661	CUUCGCCUUAUCUCCUUG	1357
CAUGUCACGAACGACUUGCUC	662	CAUGUCACGAACGACUUGCUC	662	AGCAGUCGUUCGUAGACAU	1358
CAGCGGUCGAGUUCUCUGG	663	CAGCGGUCGAGUUCUCUGG	663	CCAGGAACUCGACCCGCU	1359
UUCCACUACGUGACGGGCA	664	UUCCACUACGUGACGGGCA	664	UGCCCGUACGUAUGGAA	1360
UAGGGUGGCUUCAUGCCUC	665	UAGGGUGGCUUCAUGCCUC	665	GAGGCAUGAAAGCCACCCUA	1361
UCCAGGACUGCACGUAUCU	666	UCCAGGACUGCACGUAUCU	666	AGCAUCGUGCAGUCCUGGA	1362
UCCACUACGUGACGGGCAU	667	UCCACUACGUGACGGGCAU	667	AUGCCCGUCACGUAUGGA	1363
AAUAGGGUGGCUUCAUGCC	668	AAUAGGGUGGCUUCAUGCC	668	GGCAUGAAGCCACCCUAUU	1364
GUCUUCACGGAGGCUAUGA	669	GUCUUCACGGAGGCUAUGA	669	UCAUAGCCUCCGUGAAAGAC	1365
AUAGGGUGGCUUCAUGCCU	670	AUAGGGUGGCUUCAUGCCU	670	AGGCAUGAAGCCACCCUAU	1366
UCUUCACGGAGGCUAUGAC	671	UCUUCACGGAGGCUAUGAC	671	GUCAUAGCCUCCGUGAAAG	1367
AUGCCUCAGGAAACUUGGG	672	AUGCCUCAGGAAACUUGGG	672	CCCAAGUUUCCUGAGGCAU	1368
ACCGGACGUGCUCAAGGA	673	ACCGGACGUGCUCAAGGA	673	UCCUUGAGCACGUCGCCGGU	1369
GGGGCUGUGCAGUGGAUGA	674	GGGGCUGUGCAGUGGAUGA	674	UCAUCCACUGCACAGCCCC	1370
AAGCUCCAGGACUGCACGA	675	AAGCUCCAGGACUGCACGA	675	UCGUGCAGUCCUGGAGCUU	1371
GCUCCAGGACUGCACGAUG	676	GCUCCAGGACUGCACGAUG	676	CAUCGUGCAGUCCUGGAGC	1372
UACCGGACGUGCUCAAAGG	677	UACCGGACGUGCUCAAAGG	677	CCUUGAGCACGUCGCCGUA	1373
GGGCUUGGCAUGGAUGAA	678	GGGCUUGGCAUGGAUGAA	678	UUCAUCCACUGCACAGCCCC	1374

CGUCAAGUUC CCGGGCGGU	679	CGUCAAGUUC CCGGGCGGU	679	ACCGCCGGGAACUUGACG	1375
UCAUAUAGGGUGGCUUCAUG	680	UCAUAUAGGGUGGCUUCAUG	680	CAUGAAGCCACCUCUAUUGA	1376
AGUCUUCACGGAGGCUAUG	681	AGUCUUCACGGAGGCUAUG	681	CAUAGCCUCCGUGAAGACU	1377
GGACCAAGCGGAGACGGCU	682	GGACCAAGCGGAGACGGCU	682	AGCCGUCUCCGCUUGGUCC	1378
GGCUCCAAGUCCAAGCUCCU	683	GGCUCCAAGUCCAAGCUCCU	683	AGGAGCUUGGACUGGAGCC	1379
GGCUGUGCAGUGGAUGAAC	684	GGCUGUGCAGUGGAUGAAC	684	GUUCAUCCACUGCACAGCC	1380
CUCCAGGACUGCACGAU GC	685	CUCCAGGACUGCACGAU GC	685	GCAUCGUGCAGUCCUGGAG	1381
GAGUCUUCACGGAGGCUAU	686	GAGUCUUCACGGAGGCUAU	686	AUAGCCUCCGUGAAGACUC	1382
UGGCUCCAGUCCAAGCUCC	687	UGGCUCCAGUCCAAGCUCC	687	GGAGCUUGGACUGGAGCCA	1383
GGGGAUUUCCACUACGUGA	688	GGGGAUUUCCACUACGUGA	688	UCACGUAGUGGAAAUCCCC	1384
CAUGCCUCAGGAACUUGG	689	CAUGCCUCAGGAACUUGG	689	CCAAGUUUCCUGAGGCAUG	1385
AUCAUAUAGGUGGCUUCAU	690	AUCAUAUAGGUGGCUUCAU	690	AUGAAGCCACCUCUAUUGAU	1386
GCGGGCCUUGCCUACUAUU	691	GCGGGCCUUGCCUACUAUU	691	AAUAGUAGGCAAGGCCCGC	1387
CCGGGACGUGCUCAAGGAG	692	CCGGGACGUGCUCAAGGAG	692	CUCCUUGAGCACGUCGCCGG	1388
CCAUGGUGGGGAACUGGGC	693	CCAUGGUGGGGAACUGGGC	693	GCCCAGUUC CCCCACCAUUGG	1389
CAUAAGGUGGCUUCAUGC	694	CAUAAGGUGGCUUCAUGC	694	GCAUGAAGCCACCUCUAUUG	1390
AGCUCCAGGACUGCACGAU	695	AGCUCCAGGACUGCACGAU	695	AUCGUGCAGUCCUGGAGCU	1391
CGGGCCUUGCCUACUAUUC	696	CGGGCCUUGCCUACUAUUC	696	GAUAUAGUAGGCAAGGCCCG	1392

The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhang sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhanging sequence of the lower sequence is optionally complementary to a portion of the target sequence. The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII or any combination thereof.

Table III: HCV Synthetic Modified siNA constructs

Target Pos	Target	Seq ID	Compound #	Aliases	Sequence	Seq ID
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25237	HCV IRES Loop IIIb (Heptazyme site) as siNA str1 (sense)	B GGUCCUUUCUUGGAUCAACCC B	1413
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25238	HCV IRES Loop IIIb (Heptazyme site) as siNA str2 (antisense)	B GGGUUGAUCCAAGAAAGGACC B	1414
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25251	HCV IRES Loop IIIb (Heptazyme site) as siNA str1 (sense) Inverted Control	B CCCAACUAGGUUCUUUCCUGG B	1415
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25252	HCV IRES Loop IIIb (Heptazyme site) as siNA str1 (sense) Inverted Control Complement	B CCAGGAAAGAACCUAGUUGGG B	1416
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25814	HCV IRES Loop IIIb (Heptazyme site) as siNA str1 (sense)+2U overhang	GGUCCUUUCUUGGAUCAACCCUU	1417
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25815	HCV IRES Loop IIIb (Heptazyme site) as siNA str2 (antisense) +2U overhang	GGGUUGAUCCAAGAAAGGACC UU	1418
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25834	HCV IRES Loop IIIb (Heptazyme site) as siNA str1 (sense)+2U overhang	BGGUCCUUUCUUGGAUCAACCCUUB	1419
177	GGUCCUUUCUUGGAUCAACCCGC	1393	25835	HCV IRES Loop IIIb (Heptazyme site) as siNA str2 (antisense) +2U overhang	BGGGUUGAUCCAAGAAAGGACC UUB	1420
323	UGCCCCGGGAGGUCUCGUAGACC	1394	28415	HCV-Luc:325U21 TT siNA sense	CCCCGGGAGGUCUCGUAGATT	1421
160	UGCGGAACCGGUGAGUACACCCGG	1395	28416	HCV-Luc:162U21 TT siNA sense	CGGAACCGGUGAGUACACCTT	1422
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	28417	HCV-Luc:324U21 TT siNA sense	GCCCCGGGAGGUCUCGUAGTT	1423
161	GCGGAACCGGUGAGUACACCCGA	1397	28418	HCV-Luc:163U21 TT siNA sense	GGAACCGGUGAGUACACCGTT	1424
292	UUGUGGUACUGCCUGAUAGGGUG	1398	28419	HCV-Luc:294U21 TT siNA sense	GUGGUACUGCCUGAUAGGGTT	1425
291	CUUGUGGUACUGCCUGAUAGGGU	1399	28420	HCV-Luc:293U21 TT siNA sense	UGUGGUACUGCCUGAUAGGTT	1426
290	CCUUGUGGUACUGCCUGAUAGGG	1400	28421	HCV-Luc:292U21 TT siNA sense	UUGUGGUACUGCCUGAUAGTT	1427
323	UGCCCCGGGAGGUCUCGUAGACC	1394	28422	HCV-Luc:343L21 TT siNA (325C) antisense	UCUACGAGACCUCUCCGGGTT	1428
160	UGCGGAACCGGUGAGUACACCCGG	1395	28423	HCV-Luc:180L21 TT siNA (162C) antisense	GGUGUACUCACCGGUUCCGTT	1429
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	28424	HCV-Luc:342L21 TT siNA (324C) antisense	CUACGAGACCUCUCCGGGCTT	1430
161	GCGGAACCGGUGAGUACACCCGA	1397	28425	HCV-Luc:181L21 TT siNA (163C) antisense	CGGUGUACUCACCGGUUCCCTT	1431
292	UUGUGGUACUGCCUGAUAGGGUG	1398	28426	HCV-Luc:312L21 TT siNA (294C) antisense	CCCUAUCAGGCAGUACCACATT	1432
291	CUUGUGGUACUGCCUGAUAGGGU	1399	28427	HCV-Luc:311L21 TT siNA (293C) antisense	CCU AUCAGGCAGUACCACATT	1433
290	CCUUGUGGUACUGCCUGAUAGGG	1400	28428	HCV-Luc:310L21 TT siNA (292C) antisense	CUAUCAGGCAGUACCACAATT	1434
323	UGCCCCGGGAGGUCUCGUAGACC	1394	28429	HCV-Luc:325U21 TT siNA inv sense	TTAGAUGCUCUGGAGGGCCCC	1435
160	UGCGGAACCGGUGAGUACACCCGG	1395	28430	HCV-Luc:162U21 TT siNA inv sense	TTCCACAUGAGUGGCCAAGGC	1436
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	28431	HCV-Luc:324U21 TT siNA inv sense	TTGAUGCUCUGGAGGGCCCCCG	1437
161	GCGGAACCGGUGAGUACACCCGA	1397	28432	HCV-Luc:163U21 TT siNA inv sense	TTGCCACAUGAGUGGCCAAGG	1438

292	UUUGGUACUGCCUGAUAGGGUG	1398	28433	HCV-Luc:294U21 TT siNA inv sense	TTGGGAUAGUCCGUCAUUGGUG	1439
291	CUUGUGGUACUGCCUGAUAGGGU	1399	28434	HCV-Luc:293U21 TT siNA inv sense	TTGGAUAGUCCGUCAUUGGUGU	1440
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	28435	HCV-Luc:292U21 TT siNA inv sense	TTGAUAGUCCGUCAUUGGUGUU	1441
323	UGCCCCGGGAGGUCUCGUAGACC	1394	28436	HCV-Luc:343L21 TT siNA (325C) inv antisense	TTGGGGCCCCUCCAGAGCAUCU	1442
160	UGCGGAACCGGUGAGUACACCGG	1395	28437	HCV-Luc:180L21 TT siNA (162C) inv antisense	TTGCCUUUGGCCACUCAUGUGG	1443
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	28438	HCV-Luc:342L21 TT siNA (324C) inv antisense	TTCGGGGCCCCUCCAGAGCAUC	1444
161	GCGGAACCGGUGAGUACACCGGA	1397	28439	HCV-Luc:181L21 TT siNA (163C) inv antisense	TTCCUUUGGCCACUCAUGUGGC	1445
292	UUUGUGGUACUGCCUGAUAGGGUG	1398	28440	HCV-Luc:312L21 TT siNA (294C) inv antisense	TTCACCAUGACGGACUAUCCC	1446
291	CUUGUGGUACUGCCUGAUAGGGU	1399	28441	HCV-Luc:311L21 TT siNA (293C) inv antisense	TTACACCAUGACGGACUAUCC	1447
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	28442	HCV-Luc:310L21 TT siNA (292C) inv antisense	TTAACACCAUGACGGACUAUC	1448
160	UGCGGAACCGGUGAGUACACCGG	1395	29573	HCV-Luc:162U21 siNA sense	CGGAACCGGUGAGUACACCGG	1449
161	GCGGAACCGGUGAGUACACCGGA	1397	29574	HCV-Luc:163U21 siNA sense	GGAACCGGUGAGUACACCGGA	1450
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	29575	HCV-Luc:292U21 siNA sense	UUUGUGUACUGCCUGAUAGGG	1451
291	CUUGUGGUACUGCCUGAUAGGGU	1399	29576	HCV-Luc:293U21 siNA sense	UGUGGUACUGCCUGAUAGGGU	1452
292	UUUGUGGUACUGCCUGAUAGGGUG	1398	29577	HCV-Luc:294U21 siNA sense	GUGGUACUGCCUGAUAGGGUG	1453
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	29578	HCV-Luc:324U21 siNA sense	GCCCCGGAGGUCUCGUAGAC	1454
323	UGCCCCGGGAGGUCUCGUAGACC	1394	29579	HCV-Luc:325U21 siNA sense	CCCCGGGAGGUCUCGUAGACC	1455
160	UGCGGAACCGGUGAGUACACCGG	1395	29580	HCV-Luc:182L21 siNA (162C) antisense	GGUGUACUCACCGGUUCCGCA	1456
161	GCGGAACCGGUGAGUACACCGGA	1397	29581	HCV-Luc:183L21 siNA (163C) antisense	CGGUGUACUCACCGGUUCCGC	1457
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	29582	HCV-Luc:312L21 siNA (292C) antisense	CUAUCAGGCAGUACCAACAA	1458
291	CUUGUGGUACUGCCUGAUAGGGU	1399	29583	HCV-Luc:313L21 siNA (293C) antisense	CCUAUCAGGCAGUACCAACAG	1459
292	UUUGUGGUACUGCCUGAUAGGGUG	1398	29584	HCV-Luc:314L21 siNA (294C) antisense	CCCUAUCAGGCAGUACCAACAA	1460
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	29585	HCV-Luc:344L21 siNA (324C) antisense	CUACGAGACCUCUCCGGGGCAC	1461
323	UGCCCCGGGAGGUCUCGUAGACC	1394	29586	HCV-Luc:345L21 siNA (325C) antisense	UCUACGAGACCUCUCCGGGGCA	1462
160	UGCGGAACCGGUGAGUACACCGG	1395	29587	HCV-Luc:162U21 siNA inv sense	GGCCACAUGAGUGGCCCAAGGC	1463
161	GCGGAACCGGUGAGUACACCGGA	1397	29588	HCV-Luc:163U21 siNA inv sense	AGGCCACAUGAGUGGCCCAAGG	1464
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	29589	HCV-Luc:292U21 siNA inv sense	GGGAUAGUCCGUCAUUGGUGUU	1465
291	CUUGUGGUACUGCCUGAUAGGGU	1399	29590	HCV-Luc:293U21 siNA inv sense	UGGGAUAGUCCGUCAUUGGUGU	1466
292	UUUGUGGUACUGCCUGAUAGGGUG	1398	29591	HCV-Luc:294U21 siNA inv sense	GUGGGAUAGUCCGUCAUUGGUG	1467
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	29592	HCV-Luc:324U21 siNA inv sense	CAGAUGCUCUGGAGGCCCCCG	1468
323	UGCCCCGGGAGGUCUCGUAGACC	1394	29593	HCV-Luc:325U21 siNA inv sense	CCAGAUGCUCUGGAGGCCCCCG	1469
160	UGCGGAACCGGUGAGUACACCGG	1395	29594	HCV-Luc:182L21 siNA (162C) inv antisense	ACGCCUUUGGCCACUCAUGUGG	1470
161	GCGGAACCGGUGAGUACACCGGA	1397	29595	HCV-Luc:183L21 siNA (163C) inv antisense	CGCCUUUGGCCACUCAUGUGGC	1471
290	CCUUUGUGGUACUGCCUGAUAGGG	1400	29596	HCV-Luc:312L21 siNA (292C) inv antisense	GGAACACCAUGACGGACUAUC	1472
291	CUUGUGGUACUGCCUGAUAGGGU	1399	29597	HCV-Luc:313L21 siNA (293C) inv antisense	GAACACCAUGACGGACUAUCC	1473
292	UUUGUGGUACUGCCUGAUAGGGUG	1398	29598	HCV-Luc:314L21 siNA (294C) inv antisense	AACACCAUGACGGACUAUCCC	1474



322	GUGCCCCGGGAGGUCUCGUAGAC	1396	29599	HCV-Luc:344L21 siNA (324C) inv antisense	CACGGGGCCCUCCAGAGCAUC	1475
323	UGCCCCCGGAGGUCUCGUAGACC	1394	29600	HCV-Luc:345L21 siNA (325C) inv antisense	ACGGGGCCCUCCAGAGCAUCU	1476
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30051	HCV-Luc:325U21 siNA 5' P=S + 3' univ. base 2 + 5'/3' invAba sense	BCsCsCsCsGsGGAGGUCUCGUAGAXXB	1477
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30052	HCV-Luc:325U21 siNA inv 5' P=S + 3' univ. base 2 + 5'/3' invAba sense	BAsgsAsUsGsCUCUGGAGGGCCCCXXB	1478
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30053	HCV-Luc:345L21 siNA (325C) 5' P=S + 3' univ. base 2 + 3' invAba antisense	UsCsUsAsCsGAGACCUCCCCGGGXXB	1479
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30054	HCV-Luc:345L21 siNA (325C) inv 5' P=S + 3' univ. base 2 + 3' invAba antisense	GsGsGsGsCsCCUCCAGAGCAUCUXXB	1480
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30055	HCV-Luc:325U21 siNA all Y P=S + 3' univ. base 2 + 5'/3' invAba sense	BCsCsCsCsGGGAGGUsCsUsCsGUsAGA XXB	1481
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30056	HCV-Luc:325U21 siNA inv all Y P=S + 3' univ. base 2 + 5'/3' invAba sense	BAGAUsgCsUsCsUsGGAGGGCsCsCsCs XXB	1482
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30057	HCV-Luc:345L21 siNA (325C) all Y P=S + 3' univ. base 2 + 3' invAba antisense	UsCsUsACsGAGACsCsUsCsCsCsGGGG XXB	1483
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30058	HCV-Luc:345L21 siNA (325C) inv all Y P=S + 3' univ. base 2 + 3' invAba antisense	GGGGCsCsCsUsCsCsAGAGCsAUscsUs XXB	1484
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30059	HCV-Luc:325U21 siNA 4/3 P=S ends + all Y-2'F + 3' univ. base 2 + 5'/3' invAba sense	BcscscscsGGGAGGucucGuAsGsAsXXB	1485
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30060	HCV-Luc:325U21 siNA inv 4/3 P=S ends + all Y-2'F + 3' univ. base 2 + 5'/3' invAba sense	BAsgsAsusGcucuGGAGGGccscscsXXB	1486
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30170	HCV-Luc:325U21 siNA all Y-2'F + 3' univ. base 2 + 5'/3' invAba sense	B ccccGGGAGGucucGuAGAXX B	1487
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30171	HCV-Luc:325U21 siNA inv all Y-2'F + 3' univ. base 2 + 5'/3' invAba sense	B AGAUgucucuGGAGGGccccXX B	1488
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30172	HCV-Luc:345L21 siNA (325C) all Y P=S + 3' univ. base 2 + 5'/3' invAba antisense	B UsCsUsACsGAGACsCsUsCsCsCsGGGG XX B	1489
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30173	HCV-Luc:345L21 siNA (325C) all Y-2'F antisense	ucuAcGAGAccucccGGGG	1490
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30175	HCV-Luc:345L21 siNA (325C) all Y-2'F + 3' univ. base 2 antisense	ucuAcGAGAccucccGGGGXX	1491
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30176	HCV-Luc:345L21 siNA (325C) inv all Y-2'F + 3' univ. base 2 antisense	GGGGccccuccAGAGcAucuxX	1492
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30177	HCV-Luc:345L21 siNA (325C) all Y-2'F + 3' univ. base 2 + 5'/3' IB antisense	B ucuAcGAGAccucccGGGGXX B	1493
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30178	HCV-Luc:325U21 siNA all Y P=S + 3' univ. base 2 + 3' invAba sense	CsCsCsCsGGGAGGUsCsUsCsGUsAGAX X B	1494
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30417	HCV-Luc:325U21 siNA w/IB sense	CCCCGGGAGGUCUCGUAGACC B	1495
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30418	HCV-Luc:325U21 siNA w/IB sense	B CCCCCGGGAGGUCUCGUAGACC B	1496
323	UGCCCCCGGAGGUCUCGUAGACC	1394	30419	HCV-Luc:345L21 siNA (325C) w/IB antisense	UCUACGAGACCUCCCCGGGCA B	1497



323	UGCCCCGGGAGGUCUCGUAGACC	1394	30420	HCV-Luc:345L21 siNA (325C) w/IB antisense	B UCUACGAGACCCUCCCGGGGCA B	1498
323	UGCCCCGGGAGGUCUCGUAGACC	1394	30561	HCV-Luc:325U21 siNA Y-2'OMe (stab06) + 5'/3' invAba sense	BccccGGGAGGucucGuAGATTB	1499
323	UGCCCCGGGAGGUCUCGUAGACC	1394	30562	HCV-Luc:345L21 siNA (325C) Y-2'F, R-2'OMe + TsT antisense	ucuAcGAGAccuccccGGGGTsT	1500
151	AUAGUGGUCUGCGGAACCGGUGA	1401	30649	HCV-Luc:153U21 siNA stab07 sense	B AGUGGucucGcGGAAccGGuTT B	1501
157	GUCUGCGGAACCGGUGAGUACAC	1402	30650	HCV-Luc:159U21 siNA stab07 sense	B cuGcGGAACcGGuGAGuAcTT B	1502
289	GCCUUGUGGUACUGCCUGAUAGG	1403	30651	HCV-Luc:291U21 siNA stab07 sense	B cuuGuGGuAcuGccuGAuATT B	1503
293	UGUGGUACUGCCUGAUAGGGUGC	1404	30652	HCV-Luc:295U21 siNA stab07 sense	B uGGuAcuGccuGAuAGGGuTT B	1504
294	GUGGUACUGCCUGAUAGGGUGCU	1405	30653	HCV-Luc:296U21 siNA stab07 sense	B GGUAcuGccuGAuAGGGuGTT B	1505
295	UGGUACUGCCUGAUAGGGUGCUU	1406	30654	HCV-Luc:297U21 siNA stab07 sense	B GuAcuGccuGAuAGGGuGcTT B	1506
296	GGUACUGCCUGAUAGGGUGCUUG	1407	30655	HCV-Luc:298U21 siNA stab07 sense	B uAcuGccuGAuAGGGuGcuTT B	1507
298	UACUGCCUGAUAGGGUGCUUGCG	1408	30656	HCV-Luc:300U21 siNA stab07 sense	B cuGccuGAuAGGGuGcuuGTT B	1508
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	30657	HCV-Luc:301U21 siNA stab07 sense	B uGccuGAuAGGGuGcuuGcTT B	1509
301	UGCCUGAUAGGGUGCUUGCGAGU	1410	30658	HCV-Luc:303U21 siNA stab07 sense	B ccuGAuAGGGuGcuuGcGATT B	1510
304	CUGAUAGGGUGCUUGCGAGUGCC	1411	30659	HCV-Luc:306U21 siNA stab07 sense	B GAuAGGGuGcuuGcGAGuGTT B	1511
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	30660	HCV-Luc:324U21 siNA stab07 sense	B GccccGGGAGGucucGuAGTT B	1512
151	AUAGUGGUCUGCGGAACCGGUGA	1401	30661	HCV-Luc:173L21 siNA (153C) stab08 antisense	AccGGuuccGcAGAccAcuTsT	1513
157	GUCUGCGGAACCGGUGAGUACAC	1402	30662	HCV-Luc:179L21 siNA (159C) stab08 antisense	GuAcucAccGGuuccGcAGTsT	1514
289	GCCUUGUGGUACUGCCUGAUAGG	1403	30663	HCV-Luc:311L21 siNA (291C) stab08 antisense	uAucAGGcAGuAccAcAGTsT	1515
293	UGUGGUACUGCCUGAUAGGGUGC	1404	30664	HCV-Luc:315L21 siNA (295C) stab08 antisense	AcccuAucAGGcAGuAccATsT	1516
294	GUGGUACUGCCUGAUAGGGUGCU	1405	30665	HCV-Luc:316L21 siNA (296C) stab08 antisense	cAcccuAucAGGcAGuAccTsT	1517
295	UGGUACUGCCUGAUAGGGUGCUU	1406	30666	HCV-Luc:317L21 siNA (297C) stab08 antisense	GcAcccuAucAGGcAGuAcTsT	1518
296	GGUACUGCCUGAUAGGGUGCUUG	1407	30667	HCV-Luc:318L21 siNA (298C) stab08 antisense	AGcAcccuAucAGGcAGuATsT	1519
298	UACUGCCUGAUAGGGUGCUUGCG	1408	30668	HCV-Luc:320L21 siNA (300C) stab08 antisense	cAAGcAcccuAucAGGcAGTsT	1520
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	30669	HCV-Luc:321L21 siNA (301C) stab08 antisense	GcAAGcAcccuAucAGGcATsT	1521
301	UGCCUGAUAGGGUGCUUGCGAGU	1410	30670	HCV-Luc:323L21 siNA (303C) stab08 antisense	ucGcAAGcAcccuAucAGGTsT	1522
304	CUGAUAGGGUGCUUGCGAGUGCC	1411	30671	HCV-Luc:326L21 siNA (306C) stab08 antisense	cAcucGcAAGcAcccuAucTsT	1523
322	GUGCCCCGGGAGGUCUCGUAGAC	1396	30672	HCV-Luc:344L21 siNA (324C) stab08 antisense	cuAcGAGAccuccccGGGGcTsT	1524
151	AUAGUGGUCUGCGGAACCGGUGA	1401	30673	HCV-Luc:153U21 siNA stab07 inv sense	B uGGccAAGGcGucGGuGATT B	1525
157	GUCUGCGGAACCGGUGAGUACAC	1402	30674	HCV-Luc:159U21 siNA stab07 inv sense	B cAuGAGuGGccAAGGcGucTT B	1526
289	GCCUUGUGGUACUGCCUGAUAGG	1403	30675	HCV-Luc:291U21 siNA stab07 inv sense	B AuAGuccGucAuGGuGuucTT B	1527
293	UGUGGUACUGCCUGAUAGGGUGC	1404	30676	HCV-Luc:295U21 siNA stab07 inv sense	B uGGGAuAGuccGucAuGGuTT B	1528
294	GUGGUACUGCCUGAUAGGGUGCU	1405	30677	HCV-Luc:296U21 siNA stab07 inv sense	B GuGGGAuAGuccGucAuGGTT B	1529
295	UGGUACUGCCUGAUAGGGUGCUU	1406	30678	HCV-Luc:297U21 siNA stab07 inv sense	B cGuGGGAuAGuccGucAuGTT B	1530
296	GGUACUGCCUGAUAGGGUGCUUG	1407	30679	HCV-Luc:298U21 siNA stab07 inv sense	B ucGuGGGAuAGuccGucAuTT B	1531

298	UACUGCCUGAUAGGGUGCUUGCG	1408	30680	HCV-Luc:300U21 siNA stab07 inv sense	B GuucGuGGGAuAGuccGucTT B	1532
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	30681	HCV-Luc:301U21 siNA stab07 inv sense	B cGuucGuGGGAuAGuccGuTT B	1533
301	UGCCUGAUAGGGUGCUUGCGAGU	1410	30682	HCV-Luc:303U21 siNA stab07 inv sense	B AGcGuucGuGGGAuAGuccTT B	1534
304	CUGAUAGGGUGCUUGCGAGUGCC	1411	30683	HCV-Luc:306U21 siNA stab07 inv sense	B GuGAGcGuucGuGGGAuAGTT B	1535
322	GUGCCCCGGAGGUCUCGUAGAC	1396	30684	HCV-Luc:324U21 siNA stab07 inv sense	B GAuGcucuGGAGGGGccccGTT B	1536
151	AUAGUGGUCUGCGGAACCGGUGA	1401	30685	HCV-Luc:173L21 siNA (153C) stab08 inv antisense	ucAccAGAcGccuuGGccATsT	1537
157	GUCUGCGGAACCGGUGAGUACAC	1402	30686	HCV-Luc:179L21 siNA (159C) stab08 inv antisense	GAcGccuuGGccAcucAuGTsT	1538
289	GCCUUGUGGUACUGCCUGAUAGG	1403	30687	HCV-Luc:311L21 siNA (291C) stab08 inv antisense	GAACAccAuGAcGGAcuAuTsT	1539
293	UGUGGUACUGCCUGAUAGGGUGC	1404	30688	HCV-Luc:315L21 siNA (295C) stab08 inv antisense	AccAuGAcGGAcuAucccATsT	1540
294	GUGGUACUGCCUGAUAGGGUGCU	1405	30689	HCV-Luc:316L21 siNA (296C) stab08 inv antisense	ccAuGAcGGAcuAucccAcTsT	1541
295	UGGUACUGCCUGAUAGGGUGCUU	1406	30690	HCV-Luc:317L21 siNA (297C) stab08 inv antisense	cAuGAcGGAcuAucccAcGTsT	1542
296	GGUACUGCCUGAUAGGGUGCUUG	1407	30691	HCV-Luc:318L21 siNA (298C) stab08 inv antisense	AuGAcGGAcuAucccAcGATsT	1543
298	UACUGCCUGAUAGGGUGCUUGCG	1408	30692	HCV-Luc:320L21 siNA (300C) stab08 inv antisense	GAcGGAcuAucccAcGAAcTsT	1544
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	30693	HCV-Luc:321L21 siNA (301C) stab08 inv antisense	AcGGAcuAucccAcGAAcGTsT	1545
301	UGCCUGAUAGGGUGCUUGCGAGU	1410	30694	HCV-Luc:323L21 siNA (303C) stab08 inv antisense	GGAcuAucccAcGAAcGcuTsT	1546
304	CUGAUAGGGUGCUUGCGAGUGCC	1411	30695	HCV-Luc:326L21 siNA (306C) stab08 inv antisense	cuAucccAcGAAcGcucAcTsT	1547
322	GUGCCCCGGAGGUCUCGUAGAC	1396	30696	HCV-Luc:344L21 siNA (324C) stab08 inv antisense	cGGGGccccuccAGAGcAucTsT	1548
323	UGCCCCGGAGGUCUCGUAGACC	1394	31340	HCV-Luc:325U21 siNA stab04 sense	B ccccGGGAGGucucGuAGATT B	1549
323	UGCCCCGGAGGUCUCGUAGACC	1394	31341	HCV-Luc:325U21 siNA inv stab04 sense	B AGAuGcucuGGAGGGccccTT B	1550
323	UGCCCCGGAGGUCUCGUAGACC	1394	31342	HCV-Luc:345L21 siNA (325C) stab05 antisense	ucuAcGAGAccucccGGGGTsT	1551
323	UGCCCCGGAGGUCUCGUAGACC	1394	31343	HCV-Luc:345L21 siNA (325C) inv stab05 antisense	GGGGccccuccAGAGcAucTsT	1552
323	UGCCCCGGAGGUCUCGUAGACC	1394	31344	HCV-Luc:325U21 siNA stab07 sense	B ccccGGGAGGucucGuAGATT B	1553
323	UGCCCCGGAGGUCUCGUAGACC	1394	31345	HCV-Luc:325U21 siNA inv stab07 sense	B AGAuGcucuGGAGGGccccTT B	1554
323	UGCCCCGGAGGUCUCGUAGACC	1394	31346	HCV-Luc:345L21 siNA (325C) inv stab08 antisense	GGGGccccuccAGAGcAucTsT	1555
323	UGCCCCGGAGGUCUCGUAGACC	1394	31347	HCV-Luc:345L21 siNA (325C) stab11 antisense	ucuAcGAGAccucccGGGGTsT	1556
323	UGCCCCGGAGGUCUCGUAGACC	1394	31348	HCV-Luc:345L21 siNA (325C) inv stab11 antisense	GGGGccccuccAGAGcAucTsT	1557

151	AUAGUGGUCUGCGGAACCGGUGA	1401	31453	HCV-Luc:153U21 siNA stab04 sense	B AGuGGucUcGcGGAaccGGuTT B	1558
157	GUCUGCGGAACCGGUGAGUACAC	1402	31454	HCV-Luc:159U21 siNA stab04 sense	B cuGcGGAAccGGuGAGuAcTT B	1559
285	AAAGCCUUGUGGUACUGCCUGA	1412	31455	HCV-Luc:287U21 siNA stab04 sense	B AGGccuuGUGGuAcuGccuTT B	1560
289	GCCUUGUGGUACUGCCUGAUAGG	1403	31456	HCV-Luc:291U21 siNA stab04 sense	B cuuGuGGuAcuGccuGAuATT B	1561
293	UGUGGUACUGCCUGAUAGGGUGC	1404	31457	HCV-Luc:295U21 siNA stab04 sense	B uGGuAcuGccuGAuAGGGuTT B	1562
294	GUGGUACUGCCUGAUAGGGUGCU	1405	31458	HCV-Luc:296U21 siNA stab04 sense	B GGuAcuGccuGAuAGGGuGTT B	1563
295	UGGUACUGCCUGAUAGGGUGCUU	1406	31459	HCV-Luc:297U21 siNA stab04 sense	B GuAcuGccuGAuAGGGuGcTT B	1564
296	GGUACUGCCUGAUAGGGUGCUUG	1407	31460	HCV-Luc:298U21 siNA stab04 sense	B uAcuGccuGAuAGGGuGcuTT B	1565
298	UACUGCCUGAUAGGGUGCUUGCG	1408	31461	HCV-Luc:300U21 siNA stab04 sense	B cuGccuGAuAGGGuGcuuGTT B	1566
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	31462	HCV-Luc:301U21 siNA stab04 sense	B uGccuGAuAGGGuGcuuGcTT B	1567
301	UGCCUGAUAGGGUGCUUUGCGAGU	1410	31463	HCV-Luc:303U21 siNA stab04 sense	B ccuGAuAGGGuGcuuGcGATT B	1568
304	CUGAUAGGGUGCUUUGCGAGGCC	1411	31464	HCV-Luc:306U21 siNA stab04 sense	B GAuAGGGuGcuuGcGAGuGTT B	1569
151	AUAGUGGUCUGCGGAACCGGUGA	1401	31465	HCV-Luc:173L21 siNA (153C) stab05 antisense	AccGGuuccGcAGAccAcuTsT	1570
157	GUCUGCGGAACCGGUGAGUACAC	1402	31466	HCV-Luc:179L21 siNA (159C) stab05 antisense	GuAcucAccGGuuccGcAGTsT	1571
285	AAAGCCUUGUGGUACUGCCUGA	1412	31467	HCV-Luc:307L21 siNA (287C) stab05 antisense	AGGAGuAccAcAAAGGccuTsT	1572
289	GCCUUGUGGUACUGCCUGAUAGG	1403	31468	HCV-Luc:311L21 siNA (291C) stab05 antisense	uAucAGGcAGuAccAcAAAGTsT	1573
293	UGUGGUACUGCCUGAUAGGGUGC	1404	31469	HCV-Luc:315L21 siNA (295C) stab05 antisense	AcccuAucAGGcAGuAccATsT	1574
294	GUGGUACUGCCUGAUAGGGUGCU	1405	31470	HCV-Luc:316L21 siNA (296C) stab05 antisense	cAcccuAucAGGcAGuAccTsT	1575
295	UGGUACUGCCUGAUAGGGUGCUU	1406	31471	HCV-Luc:317L21 siNA (297C) stab05 antisense	GcAcccuAucAGGcAGuAcTsT	1576
296	GGUACUGCCUGAUAGGGUGCUUG	1407	31472	HCV-Luc:318L21 siNA (298C) stab05 antisense	AGcAcccuAucAGGcAGuATsT	1577
298	UACUGCCUGAUAGGGUGCUUGCG	1408	31473	HCV-Luc:320L21 siNA (300C) stab05 antisense	cAAGcAcccuAucAGGcAGTsT	1578
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	31474	HCV-Luc:321L21 siNA (301C) stab05 antisense	GcAAGcAcccuAucAGGcATsT	1579
301	UGCCUGAUAGGGUGCUUUGCGAGU	1410	31475	HCV-Luc:323L21 siNA (303C) stab05 antisense	ucGcAAAGcAcccuAucAGGTsT	1580
304	CUGAUAGGGUGCUUUGCGAGGCC	1411	31476	HCV-Luc:326L21 siNA (306C) stab05 antisense	cAcucGcAAAGcAcccuAucTsT	1581
151	AUAGUGGUCUGCGGAACCGGUGA	1401	31477	HCV-Luc:153U21 siNA inv stab04 sense	B uGGccAAAGGcGucuGGuGATT B	1582
157	GUCUGCGGAACCGGUGAGUACAC	1402	31478	HCV-Luc:159U21 siNA inv stab04 sense	B cAuGAGuGGccAAGGcGucTT B	1583
285	AAAGCCUUGUGGUACUGCCUGA	1412	31479	HCV-Luc:287U21 siNA inv stab04 sense	B uccGucAuGGuGuuccGGATT B	1584
289	GCCUUGUGGUACUGCCUGAUAGG	1403	31480	HCV-Luc:291U21 siNA inv stab04 sense	B AuAGuccGucAuGGuGuucTT B	1585
293	UGUGGUACUGCCUGAUAGGGUGC	1404	31481	HCV-Luc:295U21 siNA inv stab04 sense	B uGGGAuAGuccGucAuGGuTT B	1586
294	GUGGUACUGCCUGAUAGGGUGCU	1405	31482	HCV-Luc:296U21 siNA inv stab04 sense	B GuGGGAuAGuccGucAuGGTT B	1587
295	UGGUACUGCCUGAUAGGGUGCUU	1406	31483	HCV-Luc:297U21 siNA inv stab04 sense	B cGuGGGAuAGuccGucAuGTT B	1588
296	GGUACUGCCUGAUAGGGUGCUUG	1407	31484	HCV-Luc:298U21 siNA inv stab04 sense	B ucGuGGGAuAGuccGucAuTT B	1589
298	UACUGCCUGAUAGGGUGCUUGCG	1408	31485	HCV-Luc:300U21 siNA inv stab04 sense	B GuucGuGGGAuAGuccGucTT B	1590
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	31486	HCV-Luc:301U21 siNA inv stab04 sense	B cGuucGuGGGAuAGuccGuTT B	1591
301	UGCCUGAUAGGGUGCUUUGCGAGU	1410	31487	HCV-Luc:303U21 siNA inv stab04 sense	B AGcGuucGuGGGAuAGuccTT B	1592
304	CUGAUAGGGUGCUUUGCGAGGCC	1411	31488	HCV-Luc:306U21 siNA inv stab04 sense	B GuGAGcGuucGuGGGAuAGTT B	1593



151	AUAGUGGUCUGCGGAACCGGUGA	1401	31489	HCV-Luc:173L21 siNA (153C) inv stab05 antisense	ucAccAGAcGccuuGGccATsT	1594
157	GUCUGCGGAACCGGUGAGUACAC	1402	31490	HCV-Luc:179L21 siNA (159C) inv stab05 antisense	GAcGccuuGGccAcucAuGTsT	1595
285	AAAGGCCUUGUGGUACUGCCUGA	1412	31491	HCV-Luc:307L21 siNA (287C) inv stab05 antisense	uccGGAAcAccAuGAcGGATsT	1596
289	GCCUUGUGGUACUGCCUGAUAGG	1403	31492	HCV-Luc:311L21 siNA (291C) inv stab05 antisense	GAcAccAuGAcGGAcuAuTsT	1597
293	UGUGGUACUGCCUGAUAGGGUGC	1404	31493	HCV-Luc:315L21 siNA (295C) inv stab05 antisense	AccAuGAcGGAcuAucccATsT	1598
294	GUGGUACUGCCUGAUAGGGUGCU	1405	31494	HCV-Luc:316L21 siNA (296C) inv stab05 antisense	ccAuGAcGGAcuAucccAcTsT	1599
295	UGGUACUGCCUGAUAGGGUGCUU	1406	31495	HCV-Luc:317L21 siNA (297C) inv stab05 antisense	cAuGAcGGAcuAucccAcGTsT	1600
296	GGUACUGCCUGAUAGGGUGCUUG	1407	31496	HCV-Luc:318L21 siNA (298C) inv stab05 antisense	AuGAcGGAcuAucccAcGATsT	1601
298	UACUGCCUGAUAGGGUGCUUGCG	1408	31497	HCV-Luc:320L21 siNA (300C) inv stab05 antisense	GAcGGAcuAucccAcGAAcTsT	1602
299	ACUGCCUGAUAGGGUGCUUGCGA	1409	31498	HCV-Luc:321L21 siNA (301C) inv stab05 antisense	AcGGAcuAucccAcGAAcGTsT	1603
301	UGCCUGAUAGGGUGCUUGCGAGU	1410	31499	HCV-Luc:323L21 siNA (303C) inv stab05 antisense	GGAcuAucccAcGAAcGcuTsT	1604
304	CUGAUAGGGUGCUUGCGAGUGCC	1411	31500	HCV-Luc:326L21 siNA (306C) inv stab05 antisense	cuAucccAcGAAcGcucAcTsT	1605
0	GGGUCCUUUCUUGGAUCAACCCG	1606	31659	HCVb:190U21 siNA stab04 sense	B GuccuuuuuGGAuCAAccTT B	1613
0	GGUCCUUUCUUGGAUCAACCCGC	1393	31660	HCVb:191U21 siNA stab04 sense	B uccuuuuuGGAuCAAccTT B	1614
0	CGGUCCUUUCUUGGAUCAACCC	1607	31661	HCVb:189U21 siNA stab04 sense	B GGuccuuuuuGGAUCAAcTT B	1615
0	GACCGGUCCUUUCUUGGAUCAAA	1608	31662	HCVb:186U21 siNA stab04 sense	B ccGGGuccuuuuuGGAucTT B	1616
0	GGGUCCUUUCUUGGAUCAACCCG	1606	31663	HCVb:208L21 siNA (190C) stab05 antisense	GGuuGAuccAAAGAAAGGAcTsT	1617
0	GGUCCUUUCUUGGAUCAACCCGC	1393	31664	HCVb:209L21 siNA (191C) stab05 antisense	GGGuuGAuccAAAGAAAGGATsT	1618
0	CGGUCCUUUCUUGGAUCAACCC	1607	31665	HCVb:207L21 siNA (189C) stab05 antisense	GuuGAuccAAAGAAAGGAcTsT	1619
0	GACCGGUCCUUUCUUGGAUCAAA	1608	31666	HCVb:204L21 siNA (186C) stab05 antisense	GAuccAAGAAAGGAcGcGTTsT	1620
0	GGGUCCUUUCUUGGAUCAACCCG	1606	31667	HCVb:190U21 siNA inv stab04 sense	B ccAAcuAGGuuuuuuuGTT B	1621
0	GGUCCUUUCUUGGAUCAACCCGC	1393	31668	HCVb:191U21 siNA inv stab04 sense	B cccAAcuAGGuuuuuuuGTT B	1622
0	CGGUCCUUUCUUGGAUCAACCC	1607	31669	HCVb:189U21 siNA inv stab04 sense	B cAAcuAGGuuuuuuuGTT B	1623
0	GACCGGUCCUUUCUUGGAUCAAA	1608	31670	HCVb:186U21 siNA inv stab04 sense	B cuAGGuuuuuuuGcGcTT B	1624
0	GGGUCCUUUCUUGGAUCAACCCG	1606	31671	HCVb:208L21 siNA (190C) inv stab05 antisense	cAGGAAAGAAAccuAGuuGGTsT	1625
0	GGUCCUUUCUUGGAUCAACCCGC	1393	31672	HCVb:209L21 siNA (191C) inv stab05 antisense	AGGAAAGAAAccuAGuuGGTsT	1626
0	CGGUCCUUUCUUGGAUCAACCC	1607	31673	HCVb:207L21 siNA (189C) inv stab05 antisense	ccAGGAAAGAAAccuAGuuGTsT	1627

0	GACCGGGUCCUUUCUUGGAUCAA	1608	31674	HCVb:204L21 siNA (186C) inv stab05 antisense	GGcccAGGAAAGAAccuAGTsT	1628
0	GCCCCGGAGGUCUCUGUAGACCG	1609	31702	HCVa:326U21 siNA stab07 sense	B cccGGGAGGucucGuAGAcTT B	1629
0	CCCCGGAGGUCUCUGUAGACCGU	1610	31703	HCVa:327U21 siNA stab07 sense	B ccGGGAGGucucGuAGAccTT B	1630
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31704	HCVa:328U21 siNA stab07 sense	B cGGGAGGucucGuAGAccGTT B	1631
0	CCGGAGGUCUCUGUAGACCGUGC	1612	31705	HCVa:329U21 siNA stab07 sense	B GGGAGGucucGuAGAccGuTT B	1632
0	GCCCCGGAGGUCUCUGUAGACCG	1609	31706	HCVa:344L21 siNA (326C) stab08 antisense	GucuAcGAGAccucccccGGTsT	1633
0	CCCCGGAGGUCUCUGUAGACCGU	1610	31707	HCVa:345L21 siNA (327C) stab08 antisense	GGucuAcGAGAccucccccGGTsT	1634
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31708	HCVa:346L21 siNA (328C) stab08 antisense	cGGucuAcGAGAccucccccGGTsT	1635
0	CCGGAGGUCUCUGUAGACCGUGC	1612	31709	HCVa:347L21 siNA (329C) stab08 antisense	AcGGucuAcGAGAccucccccTsT	1636
0	GCCCCGGAGGUCUCUGUAGACCG	1609	31710	HCVa:326U21 siNA inv stab07 sense	B cAGAUGcucuGGAGGGcccTT B	1637
0	CCCCGGAGGUCUCUGUAGACCGU	1610	31711	HCVa:327U21 siNA inv stab07 sense	B ccAGAUGcucuGGAGGGcccTT B	1638
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31712	HCVa:328U21 siNA inv stab07 sense	B GccAGAUGcucuGGAGGGGcTT B	1639
0	CCGGAGGUCUCUGUAGACCGUGC	1612	31713	HCVa:329U21 siNA inv stab07 sense	B uGccAGAUGcucuGGAGGGGTT B	1640
0	GCCCCGGAGGUCUCUGUAGACCG	1609	31714	HCVa:344L21 siNA (326C) inv stab08 antisense	GGGccccuccAGAGcAucuGTsT	1641
0	CCCCGGAGGUCUCUGUAGACCGU	1610	31715	HCVa:345L21 siNA (327C) inv stab08 antisense	GGccccuccAGAGcAucuGGTsT	1642
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31716	HCVa:346L21 siNA (328C) inv stab08 antisense	GccccuccAGAGcAucuGGcTsT	1643
0	CCGGAGGUCUCUGUAGACCGUGC	1612	31717	HCVa:347L21 siNA (329C) inv stab08 antisense	ccccuccAGAGcAucuGGcATsT	1644
0	GCCUUGUGGUACUGCCUGAUAGG	1403	31762	HCVa:291U21 siNA stab08 sense	cuuGuGuAuGccuGccuGAuATsT	1645
0	UGUGGUACUGCCUGAUAGGGUGC	1404	31763	HCVa:295U21 siNA stab08 sense	uGGuAuGccuGAuAGGGGuTsT	1646
0	UGCCCCGGAGGUCUCUGUAGACC	1394	31764	HCVa:325U21 siNA stab08 sense	ccccGGGAGGucucGuAGATsT	1647
0	GCCUUGUGGUACUGCCUGAUAGG	1403	31765	HCVa:291U21 siNA inv stab08 sense	AuAGuccGuAuGGuGuucTsT	1648
0	UGUGGUACUGCCUGAUAGGGUGC	1404	31766	HCVa:295U21 siNA inv stab08 sense	uGGGAuAGuccGuAuGGGuTsT	1649
0	UGCCCCGGAGGUCUCUGUAGACC	1394	31767	HCVa:325U21 siNA inv stab08 sense	AGAuGcucuGGAGGGccccTsT	1650
0	CCGGAGGUCUCUGUAGACCGUGC	1612	31709	HCVa:347L21 siNA (329C) stab08 antisense	AcGGucuAcGAGAccucccccTsT	1636
0	CCCGGAGGUCUCUGUAGACCGU	1610	31928	HCVa:327U21 siNA stab08 sense	ccGGAGGucucGuAGAccTsT	1651
0	CCCGGGAGGUCUCUGUAGACCGU	1610	31929	HCVa:327U21 siNA inv stab08 sense	ccAGAUGcucuGGAGGGGcTsT	1652
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31930	HCVa:328U21 siNA stab08 sense	cGGAGGucucGuAGAccGTsT	1653
0	CCCGGAGGUCUCUGUAGACCGUG	1611	31931	HCVa:328U21 siNA inv stab08 sense	GccAGAUGcucuGGAGGGGcTsT	1654
0	CCCGGGAGGUCUCUGUAGACCGU	1610	32007	HCVa:327U21 siNA stab08 + 5' abasic sense	B ccGGGAGGucucGuAGAccTsT	1655
0	CCCGGGAGGUCUCUGUAGACCGU	1610	32008	HCVa:327U21 siNA stab08 + 3' abasic sense	ccGGGAGGucucGuAGAccTsT B	1656
0	CCCGGGAGGUCUCUGUAGACCGU	1610	32009	HCVa:327U21 siNA stab08 + 5' & 3' abasic sense	B ccGGGAGGucucGuAGAccTsT B	1657
0	CCCCGGAGGUCUCUGUAGACCGU	1610	32174	HCVa:327 siNA 3'-classI 10bp	UCUCGUAGACCUU	1658
0	CCCCGGAGGUCUCUGUAGACCGU	1610	32175	HCVa:327 siNA 3'-classI 8bp	GGUCUACGAGACCUCCCGGTT	1659
0	CCCCGGAGGUCUCUGUAGACCGU	1610	32176	HCVa:327 siNA 3'-classI 6bp	UCGUAGACCUU	1660



							GGUCUACGAGACCUCCCGGTT		
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32177		HCVa:327 siNA 3'-classl 4bp		AGACCUU GGUCUACGAGACCUCCCGGTT	1661	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32178		HCVa:327 siNA 5'-classl 10bp		GGUCUACGAGACCUCCCGGUU CCGGAGGUCU	1662	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32179		HCVa:327 siNA 5'-classl 8bp		GGUCUACGAGACCUCCCGGUU CCGGAGGU	1663	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32180		HCVa:327 siNA 5'-classl 6bp		GGUCUACGAGACCUCCCGGUU CCGGAG	1664	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32181		HCVa:327 siNA 5'-classl 4bp		GGUCUACGAGACCUCCCGGUU CCGG	1665	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32182		HCVa:327 siNA 3'-gaaa 10bp		CUCGUAGACC GAAA GGUCUACGAGACCUCCCGGTT	1666	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32183		HCVa:327 siNA 3'-gaaa 8bp		CGUAGACC GAAA GGUCUACGAGACCUCCCGGTT	1667	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32184		HCVa:327 siNA 3'-gaaa 6bp		UAGACC GAAA GGUCUACGAGACCUCCCGGTT	1668	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32185		HCVa:327 siNA 3'-gaaa 4bp		GACC GAAA GGUCUACGAGACCUCCCGGTT	1669	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32186		HCVa:327 siNA 5'-gaaa 10bp		GGUCUACGAGACCUCCCGGUU GAAA CCGGAGGUC	1670	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32187		HCVa:327 siNA 5'-gaaa 8bp		GGUCUACGAGACCUCCCGGUU GAAA CCGGAGG	1671	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32188		HCVa:327 siNA 5'-gaaa 6bp		GGUCUACGAGACCUCCCGGUU GAAA CCGGGA	1672	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32189		HCVa:327 siNA 5'-gaaa 4bp		GGUCUACGAGACCUCCCGGUU GAAA CCGG	1673	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32190		HCVa:327 siNA 3'-uuuguguag 10bp		CGUAGACCUU UUUGUGUAG GGUCUACGAGACCUCCCGGTT	1674	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32191		HCVa:327 siNA 3'-uuuguguag 8bp		UAGACCUU UUUGUGUAG GGUCUACGAGACCUCCCGGTT	1675	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32192		HCVa:327 siNA 3'-uuuguguag 6bp		GACCUU UUUGUGUAG GGUCUACGAGACCUCCCGGTT	1676	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32193		HCVa:327 siNA 3'-uuuguguag 4bp		CCUU UUUGUGUAG GGUCUACGAGACCUCCCGGTT	1677	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32194		HCVa:327 siNA 5'-uuuguguag 10bp		GGUCUACGAGACCUCCCGGUU UUUGUGUAG CCGGAGGUC	1678	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32195		HCVa:327 siNA 5'-uuuguguag 8bp		GGUCUACGAGACCUCCCGGUU UUUGUGUAG CCGGGAGG	1679	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32196		HCVa:327 siNA 5'-uuuguguag 6bp		GGUCUACGAGACCUCCCGGUU UUUGUGUAG CCGGGA	1680	
0	CCCCGGGAGGUCUCGUAGACCGU	1610	32197		HCVa:327 siNA 5'-uuuguguag 4bp		GGUCUACGAGACCUCCCGGUU	1681	



**Table IV**

Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

<b>Chemistry</b>	<b>pyrimidine</b>	<b>Purine</b>	<b>cap</b>	<b>p=S</b>	<b>Strand</b>
“Stab 1”	Ribo	Ribo	-	5 at 5' -end 1 at 3' -end	S/AS
“Stab 2”	Ribo	Ribo	-	All linkages	Usually AS
“Stab 3”	2'-fluoro	Ribo	-	4 at 5' -end 4 at 3' -end	Usually S
“Stab 4”	2'-fluoro	Ribo	5' and 3' - ends	-	Usually S
“Stab 5”	2'-fluoro	Ribo	-	1 at 3' -end	Usually AS
“Stab 6”	2'-O-Methyl	Ribo	5' and 3' - ends	-	Usually S
“Stab 7”	2'-fluoro	2'-deoxy	5' and 3' - ends	-	Usually S
“Stab 8”	2'-fluoro	2'-O-Methyl	-	1 at 3' -end	Usually AS
“Stab 9”	Ribo	Ribo	5' and 3' - ends	-	Usually S
“Stab 10”	Ribo	Ribo	-	1 at 3' -end	Usually AS
“Stab 11”	2'-fluoro	2'-deoxy	-	1 at 3' -end	Usually AS
“Stab 12”	2'-fluoro	LNA	5' and 3' - ends		Usually S
“Stab 13”	2'-fluoro	LNA		1 at 3' -end	Usually AS
“Stab 14”	2'-fluoro	2'-deoxy		2 at 5' -end 1 at 3' -end	Usually AS
“Stab 15”	2'-deoxy	2'-deoxy		2 at 5' -end 1 at 3' -end	Usually AS
“Stab 16	Ribo	2'-O-Methyl	5' and 3' - ends		Usually S
“Stab 17”	2'-O-Methyl	2'-O-Methyl	5' and 3' -		Usually S

				ends			
“Stab 18”	2’ -fluoro	2’ -O-Methyl	5’ and 3’ -ends	1 at 3’ -end	Usually S		
“Stab 19”	Ribo	Ribo	TT at 3’ -ends		S/AS		
“Stab 20”	Ribo	Ribo	TT at 3’ -ends	1 at 3’ -end	S/AS		

CAP = any terminal cap, see for example **Figure 10**.

All Stab 1-20 chemistries can comprise 3’ -terminal thymidine (TT) residues

All Stab 1-20 chemistries typically comprise 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V

A. 2.5 μmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 μL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μL	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 μL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 μmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 μL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μL	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 μL	5 sec	5 sec	5 sec
TCA	700	732 μL	10 sec	10 sec	10 sec
Iodine	20.6	244 μL	15 sec	15 sec	15 sec
Beaucage	7.7	232 μL	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μmol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O- methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μL	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μL	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μL	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μL	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 μL	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μL	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μL	NA	NA	NA

- 5
- Wait time does not include contact time during delivery.
  - Tandem synthesis utilizes double coupling of linker molecule